

A11N, Ed Hart.

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Scientific and Technical Information Center

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SEARCH REQUEST FORM

Requester's Full Name: Celine Qian Examiner # IST 8710 Date: 9/7/05
Art Unit: 1636 Phone Number: 2-0777 Serial Number: 101030658
Location (Bldg/Room#): 2A44 (Mailbox #): 2070 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following: Mej

Title of Invention: Trap vectors and gene trapping meth. by using the sam
Inventors (please provide full names): Yamamura et al.

Earliest Priority Date: 7/14/1999

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 15 and SEQ ID NO: 16.

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TECH/CHEM. DIVISION
(STIC)

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Type of Search

Vendors and cost where applicable

Searcher: _____ ☒ NA Sequence (#)

_____ STN _____ Dialog

Searcher Phone #: _____ ☐ AA Sequence (#)

_____ Questel/Orbit _____ Lexis/Nexis

Searcher Location: _____ ☐ Structure (#)

_____ Westlaw _____ WWW/Internet

Date Searcher Picked Up: 9/8/05 ☐ Bibliographic

☒ In-house sequence systems

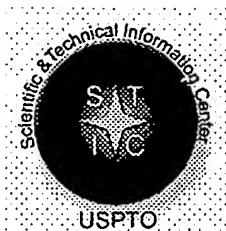
Date Completed: 9/9/05 ☐ Litigation

☒ Commercial ☐ Oligomer ☐ Score/Length
☒ Interference ☐ SPDI ☐ Encode/Transl
Other (specify) _____

Searcher Prep & Review Time: _____ ☐ Fulltext

Online Time: _____ ☐ Other

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 165067

TO: Celine Qian
Location: rem/2A64/2C70
Art Unit: 1636
Friday, September 09, 2005

Case Serial Number: 10/030658

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 21:11:18 ; Search time 797 Seconds
(without alignments)
2067.098 Million cell updates/sec

Title: US-10-030-658B-15

Perfect score: 34
Sequence: 1 tacccttgcgtatagcattacattacgaagtatt 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_stc:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	BD182868 Knockout
2	34	100.0	34	6	BD185622 Knockout
3	34	100.0	34	6	AX114843 Sequence
4	34	100.0	34	6	AX137069 Sequence
5	34	100.0	34	6	AX540640 Sequence
6	34	100.0	34	6	AX710009 Sequence
7	34	100.0	34	6	AX710011 Sequence
8	34	100.0	34	6	BD083072 Antisense
9	34	100.0	34	6	BD093611 Antisense
10	34	100.0	44	6	AX710018 Sequence
11	34	100.0	68	6	AX710014 Sequence
12	34	100.0	78	6	AX114851 Sequence
13	34	100.0	79	6	AX114852 Sequence
14	34	100.0	94	6	AX662254 Sequence
15	34	100.0	94	6	AX662260 Sequence
16	34	100.0	5054	6	BD083076 Antisense
17	34	100.0	5054	6	BD093615 Antisense
18	34	100.0	7175	6	AX114853 Sequence
19	34	100.0	8153	6	AX114871 Sequence

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21	34	100.0	9479	12	AY569778	AY569778 Cloning v
22	34	100.0	12404	12	AY569780	AY569780 Cloning v
23	32.4	95.3	34	6	AX710010	AX710010 Sequence
24	30.8	90.6	34	6	AX710012	AX710012 Sequence
25	30.8	90.6	10695	12	AY553053	AY553053 Reporter
26	30.8	90.6	53099	2	AC101086	AC101086 Mus muscu
27	30.8	90.6	46634	2	AC100010	AC100010 Mus muscu
28	30.4	89.4	65346	2	AC026597	AC026597 Homo sapi
29	30.4	89.4	71199	2	AC074079	AC074079 Homo sapi
30	30.4	89.4	74315	2	AC023029	AC023029 Homo sapi
31	30.4	89.4	80363	2	AC025805	AC025805 Homo sapi
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34	29.8	87.6	41871	2	CEH27D13	292798 Caenorhabdi
35	29.8	87.6	70835	2	AC116388	AC116388 Homo sapi
36	29.4	86.5	51500	2	AC100461	AC100461 Mus muscu
37	29.4	86.5	64036	2	AC040921	AC040921 Homo sapi
38	29.4	86.5	70984	2	AC068078	AC068078 Homo sapi
39	29.4	86.5	81967	2	AC139069	AC139069 Homo sapi
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41	29.4	86.5	89044	2	AC022633	AC022633 Homo sapi
42	29.4	86.5	89221	2	AC138746	AC138746 Homo sapi
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44	29.2	85.9	55787	2	AC090406	AC090406 Homo sapi
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ALIGNMENTS

RESULT 1	BD182868	BD182868	34 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	BD182868	Knockout animal.				
DEFINITION	BD182868	Knockout animal.				
ACCESSION	BD182868.1	GI:31875068				
VERSION	JP 2002345477-A/1					
KEYWORDS	synthetic construct					
SOURCE	synthetic construct					
ORGANISM	synthetic construct					
REFERENCE	1 (bases 1 to 34)					
AUTHORS	Ide,H., Yamamura,K. and Araki,K.					
TITLE	Knockout animal					
JOURNAL	Patent: JP 2002345477-A 1 03-DEC-2002;					
COMMENT	JAPAN SCIENCE AND TECHNOLOGY CORP,HIROYUKI IDE,KENICHI YAMAMURA, KIMI ARAKI					
	OS Artificial Sequence					
	PN JP 2002345477-A/1					
	PD 03-DEC-2002					
	PF 25-MAY-2001 JP 2001157567					
	PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI					
	PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC					
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Best Local Similarity	100.0%;	Pred. No. 0.02;		
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BD185622
LOCUS      Knockout animal.          34 bp      DNA          linear      PAT 17-JUN-2003
DEFINITION
ACCESSION  BD185622
VERSION    BD185622.1 GI:31877822
KEYWORDS  JP 2002369689-A/1.
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 34)
AUTHORS  Ide,H., Yamamura,K. and Araki,K.
TITLE     Knockout animal
JOURNAL   Patent: JP 2002369689-A 1 24-DEC-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP.EU GENE LTD, PRESIDENT OF
          KUMAMOTO UNIVERSITY
COMMENT   OS Artificial Sequence
          PN JP 2002369689-A/1
          PD 24-DEC-2002
          PP 25-MAY-2001 JP 2001157568
          PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
          PC C12N15/09,A01K67/027,C12N5/10,C12N5/00 CC
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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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DEFINITION
ACCESSION  AX114843
VERSION    AX114843.1 GI:14031785
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE     Conditional gene trapping construct for the disruption of genes
JOURNAL   Patent: WO 0129208-A 3 26-APR-2001;
          ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
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/notes="mutant loxp site - lox71"
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Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

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AX137069
LOCUS      AX137069          34 bp      DNA          linear      PAT 30-MAY-2001
DEFINITION
ACCESSION  AX137069
VERSION    AX137069.1 GI:14273414
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Kuehn,R. and von Melchner,H.
TITLE     Conditional gene trapping construct for the disruption of genes
JOURNAL   Patent: EP 1092768-A 3 18-APR-2001;
          ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
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LOCUS      AX540640          34 bp      DNA          linear      PAT 23-NOV-2002
DEFINITION
ACCESSION  AX540640
VERSION    AX540640.1 GI:25273628
KEYWORDS  .
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Xin,H.B. and Kotlikoff,M.
TITLE     Vectors for conditional gene inactivation
JOURNAL   Patent: WO 0240685-A 9 23-MAY-2002;
          CORNELL RESEARCH FOUNDATION, INC. (US)
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1
RESULT 6
AX710009
LOCUS      AX710009          34 bp      DNA          linear      PAT 10-APR-2003
DEFINITION
ACCESSION  AX710009
VERSION    AX710009.1 GI:29786620
KEYWORDS  .
SOURCE    synthetic construct

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ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Altmann,M., Neuherl,B. and Hammerschmidt,W.
TITLE Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL Patent: EP 1288295-A 6 05-MAR-2003;
GSP-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
RESULT 7
AX710011
LOCUS AX710011 34 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 8 from Patent EP1288295.
ACCESSION AX710011
VERSION AX710011.1 GI:29786622
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Altmann,M., Neuherl,B. and Hammerschmidt,W.
TITLE Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL Patent: EP 1288295-A 8 05-MAR-2003;
GSP-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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BD083072
LOCUS BD083072 34 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense type gene trap vector.
ACCESSION BD083072
VERSION BD083072.1 GI:22628682
KEYWORDS JP 2001321174-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Taniguchi,K. and Karasawa,M.
TITLE Antisense type gene trap vector
JOURNAL Patent: JP 2001321174-A 2 20-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP

OS Artificial Sequence
PN JP 2001321174-A/2
PD 20-NOV-2001
PF 11-MAY-2000 JP 2000138938
PI KATSUMI TANIGUCHI, MIKA KARASAWA
PC C12N15/09,A01K67/027,C12N5/10//C12N5/10,C12N15/00,
PC C12N5/00,
PC (C12N5/00,C12R1:91)
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Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
RESULT 9
BD093611
LOCUS BD093611 34 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense gene trap vector.
ACCESSION BD093611
VERSION BD093611.1 GI:22639199
KEYWORDS WO 0185973-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Taniguchi,M. and Karasawa,M.
TITLE Antisense gene trap vector
JOURNAL Patent: WO 0185973-A 2 15-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,MASARU TANIGUCHI,MIKA KARASAWA
COMMENT
OS Artificial Sequence
PN WO 0185973-A/2
PD 15-NOV-2001
PF 29-AUG-2000 WO 2000JP005824
PR 11-MAY-2000 JP 00P 138938
PI MASARU TANIGUCHI,MIKA KARASAWA
PC C12N15/85,C12N5/10,A01K67/027//A61K48/00
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Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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AX710018
LOCUS AX710018 44 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 15 from Patent EP1288295.
ACCESSION AX710018
VERSION AX710018.1 GI:29786629
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Altmann,M., Neuherl,B. and Hammerschmidt,W.
TITLE Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL Patent: EP 1288295-A 15 05-MAR-2003;
GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
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RESULT 11
AX710014
LOCUS AX710014 68 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 11 from Patent EP1288295.
ACCESSION AX710014
VERSION AX710014.1 GI:29786625
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Altmann,M., Neuherl,B. and Hammerschmidt,W.
TITLE Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL Patent: EP 1288295-A 15 05-MAR-2003;
GSF-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
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RESULT 12
AX114851/c
LOCUS AX114851 78 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 11 from Patent WO0129208.
ACCESSION AX114851
VERSION AX114851.1 GI:14031793
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 11 26-APR-2001;

ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
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QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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DB 78 TACCGTTCGTATAGCATACATTATACGAAGTTAT 45
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RESULT 13
AX114852
LOCUS AX114852 79 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 12 from Patent WO0129208.
ACCESSION AX114852
VERSION AX114852.1 GI:14031794
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
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AUTHORS Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 12 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
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/note="primer lox4"

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DB 6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39
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RESULT 14
AX662254
LOCUS AX662254 94 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 10 from Patent WO02083889.
ACCESSION AX662254
VERSION AX662254.1 GI:29163153
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE
1
AUTHORS Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE Methods
JOURNAL Patent: WO 02083889-A 10 24-OCT-2002;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
LOCATION/Qualifiers
1. .94
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 |||||
 Db 50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83

RESULT 15
 AX662260
 LOCUS AX662260 94 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 16 from Patent WO2083889.
 ACCESSION AX662260
 VERSION AX662260.1 GI:29163159
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Bigger,B.W., Tolmachov,O. and Coutelle,C.
 TITLE Methods
 JOURNAL Patent: WO 02083889-A 16 24-OCT-2002;
 IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
 FEATURES
 source
 1..94
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Primer"

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 |||||
 Db 50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83

Search completed: September 8, 2005, 23:38:11
 Job time : 801 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 21:09:03 ; Search time 200.5 Seconds
(without alignments)
1003.846 Million cell updates/sec

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Sequence: 1 taccgttcgtatagcattacattacgaagtat 34

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues 8780412
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980a:*
2: Geneseqn1990a:*
3: Geneseqn2000a:*
4: Geneseqn2001a:*
5: Geneseqn2001bs:*
6: Geneseqn2002a:*
7: Geneseqn2002bs:*
8: Geneseqn2003a:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004a:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	AD04917	Aad04917 Recombina
2	34	100.0	34	ABN84175	Abn84175 LoxP left
3	34	100.0	34	ABA03775	AbA03775 Synthetic
4	34	100.0	34	ABZ20929	AbZ20929 LoxP muta
5	34	100.0	34	ABZ20931	AbZ20931 LoxP muta
6	34	100.0	34	ABZ79444	AbZ79444 Lox 71 DN
7	34	100.0	34	ACC85309	Acc85309 Recombina
8	34	100.0	34	ADD13802	Add13802 Oligonuc
9	34	100.0	34	ADD15151	Add15151 Variant 1
10	34	100.0	34	ABZ75319	AbZ75319 Lox71 rel
11	34	100.0	44	ABZ20936	AbZ20936 Lox71 iso
12	34	100.0	68	ABZ20932	AbZ20932 Lox66 and
13	34	100.0	78	AD04925	Aad04925 Primer lo
14	34	100.0	79	AD04926	Aad04926 Primer lo
15	34	100.0	94	ABV75994	AbV75994 OLIGO-F
16	34	100.0	94	ABV75989	AbV75989 Oligonuc
17	34	100.0	5054	ABA03779	AbA03779 Gene trap
18	34	100.0	7175	AD04927	Aad04927 Vector pR
19	34	100.0	8153	AD04945	Aad04945 Plasmid p
20	32.4	95.3	34	ABZ20930	AbZ20930 LoxP muta

c	21	31	91.2	63	2	AAT61668	Aat61668 Chloramph
	22	30.8	90.6	34	8	ABZ20932	Abz20932 LoxP muta
	23	30.8	90.6	34	9	ACC85311	Acc85311 Recombina
	24	29	85.3	32	5	AAC92431	Aac92431 Lox P sit
	25	29	85.3	32	10	AD552399	Ad552399 LoxP site
c	26	29	85.3	34	2	AAQ47238	Aaq47238 loxp sequ
	27	29	85.3	34	2	AAQ47239	Aaq47239 loxp sequ
c	28	29	85.3	34	2	AAQ94929	Aaq94929 Wild type
c	29	29	85.3	34	2	AAT42299	Aat42299 Bacteriop
c	30	29	85.3	34	2	AAT36911	Aat36911 E. coli p
c	31	29	85.3	34	2	AAT92195	Aat92195 Bacteriop
c	32	29	85.3	34	2	AAT90585	Aat90585 Lox p rec
c	33	29	85.3	34	2	AAV17069	Aav17069 Lox P1 se
c	34	29	85.3	34	2	AAx76189	Aax76189 Variant 1
c	35	29	85.3	34	2	AAx61038	Aax61038 Yeast Lox
	36	29	85.3	34	2	AAx76039	Aax76039 5' to 3'
	37	29	85.3	34	2	AAx19902	Aax19902 Wild-type
	38	29	85.3	34	3	AAx58294	Aax58294 Bacteriop
c	39	29	85.3	34	3	AAx58293	Aax58293 Bacteriop
	40	29	85.3	34	3	AAZ58066	Aaz58066 Wild-type
c	41	29	85.3	34	3	AAx91994	Aax91994 Insert re
c	42	29	85.3	34	3	AAx10908	Aax10908 Lox site
	43	29	85.3	34	3	AAx10911	Aax10911 Lox P sit
	44	29	85.3	34	3	AAx61510	Aax61510 Nucleotid
	45	29	85.3	34	3	AAx10234	Aax10234 Bacteriop

ALIGNMENTS

RESULT 1
AAD04917
ID AAD04917 standard; DNA; 34 BP.
XX
AC AAD04917;
XX
DT 17-JUL-2001 (first entry)
XX
DE Recombinase recognition sequence (RRS), loxP site mutant (lox71) DNA.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; mutant; ds.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX WPI; 2001-308486/32.
XX
DR New gene trapping construct capable of causing conditional mutations in
XX genes, comprises functional DNA segment inserted in sense or antisense
XX direction relative to gene to be trapped.
XX
PS Claim 4; Page 49; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
XX capable of causing conditional mutations in genes. The gene trapping
XX construct comprises two functional DNA segments, each being flanked by
XX two recombinase recognition sequences (RRSs) specific to site specific

CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene
CC trapping construct is useful for mutationally inactivating all cellular
CC genes. The present DNA sequence encodes recombinase recognition sequence,
CC loxP site mutant (lox71), which flanks the functional DNA segments of
CC gene trapping construct

XX SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
Query Match 100.0%; Score 34; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||||
Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 2

ABN84175/c
ID ABN84175 standard; DNA; 34 BP.

XX AC ABN84175;

DT 23-SEP-2002 (first entry)

XX DE LoxP left element mutant.

XX KW Gene inactivation; mutagenesis; vector; knockout animal;

XX KW transgenic animal; gene trapping; loxP; mutant; ss.

XX OS Enterobacteria phage P1.

XX OS Synthetic.

XX PN WO200240685-A2.

XX PD 23-MAY-2002.

XX PF 16-NOV-2001; 2001WO-US043916.

XX PR 16-NOV-2000; 2000US-0249200P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Xin H, Kotlikoff M;

XX DR WPI; 2002-537342/57.

XX PT Novel genetically engineered vector comprising gene trap cassette, and
PT mutational element cassette that is transcriptionally silent, but which
PT is activated by recombinase expression to disrupt expression of trapped
PT gene.

XX PS Example 2; Page 35; 58pp; English.

XX CC The present invention provides recombinant vectors and methods of using
CC the vectors in a high-throughput genetic system to rapidly generate
CC conditional and/or conventional knockout mutants, e.g. in mice, useful
CC for identifying and defining mammalian gene function in vivo. The methods
CC combine gene trapping, gene targeting, and site-specific recombination
CC techniques. The vectors comprise a transcriptionally silent mutational
CC element that is inserted within a gene in a target cell in a manner that
CC retains gene function, and which can be manipulated to inactivate the
CC gene when desired. The mutational element may be flanked by mutant loxP
CC sites in a manner that produces a directional bias toward inversion of
CC the mutational sequence upon exposure to cre recombinase. Once inverted,

CC the mutational element is spliced into the trapped gene resulting in
CC expression of a reporter gene and premature termination of the endogenous
CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
CC loxP sites, a right element (RE) mutant (see ABN84176) and a left element
CC (LE) mutant (present sequence). The mutant loxP system produces a
CC reaction biased toward an irreversible gene inversion. The method of the
CC invention facilitates investigation of the function of individual genes
CC by a rapid extension of the conditional knockout approach

XX SQ Sequence 34 BP; 12 A; 5 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||||
Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 3

ABA03775

XX ID ABA03775 standard; DNA; 34 BP.

XX AC ABA03775;

XX DT 19-FEB-2002 (first entry)

XX DE Synthetic lox71 sequence.

XX KW lox71; gene therapy; gene targeting; gene trapping;

XX KW antisense RNA production; ds.

XX OS Synthetic.

XX PN WO200185973-A1.

XX PD 15-NOV-2001.

XX PF 29-AUG-2000; 2000WO-JP005824.

XX PR 11-MAY-2000; 2000JP-00138938.

XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX PI Taniguchi M, Karasawa M;

XX DR WPI; 2002-055602/07.

XX PT Antisense type gene trap vector, useful for gene therapy of diseases and
PT production of animal models for disease study, disrupts transcription of
PT specific gene.

XX PS Claim 19; Page 42; 48pp; Japanese.

XX CC The invention relates to a method for producing cells in which the
CC expression of a gene is disrupted. The cells are transformed with a gene
CC trap vector to give a trap clone having the vector inserted at a specific
CC mutation site of the target gene. The trap clone is then transformed with
CC a vector that inserts a promoter in the antisense direction of the gene,
CC enforcing transcription of antisense RNA. The method is useful for the
CC production of animal models for studying human diseases. It is also
CC useful as gene therapy for the treatment and prevention of diseases. The
CC present sequence is a lox71 sequence claimed in the specification

XX SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||||

```

Db      1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
RESULT 4
ABZ20929
ID ABZ20929 standard; DNA; 34 BP.
XX
XX AC ABZ20929;
XX
XX DT 10-APR-2003 (first entry)
XX
XX DE LoxP mutant with flanking sequence oligonucleotide #6.
XX
XX KW Non-identical recognition sequence mutant; sequence-specific recombinase;
XX recombination; antibiotic-resistance marker; loxP; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX PN DE10140030-C1.
XX
XX PD 19-DEC-2002.
XX
XX PF 16-AUG-2001; 2001DE-01040030.
XX
XX PR 16-AUG-2001; 2001DE-01040030.
XX
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
XX PI Altmann M, Neuhierl B, Hammerschmidt W;
XX
XX DR WPI; 2003-048025/05.
XX
XX PT Method for performing multiple recombination events in a genetic system,
XX useful e.g. for removing antibiotic resistance genes, uses mutant
XX recombination sites.
XX
XX PS Claim 4; Col 9; 10pp; German.
XX
XX CC The present invention relates to the use of two non-identical recognition
XX sequence mutants for a sequence-specific recombinase for performing two
XX or more recombination events, mediated by the sequence-specific
XX recombinase, in a single genetic system. The method is used to manipulate
XX genetic systems (microbial, plant or animal) by site-specific
XX recombination, e.g. to insert or remove DNA and most particularly to
XX remove antibiotic-resistance markers. The present sequence was used to
XX isolate the loxP coding sequence in the exemplification of the invention
XX
XX SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 34; DB 8; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 0.0002;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
XX
XX DB 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
XX
XX RESULT 5
XX ABZ20931
XX ID ABZ20931 standard; DNA; 34 BP.
XX
XX AC ABZ20931;
XX
XX XX DT 10-APR-2003 (first entry)
XX
XX DE LoxP mutant with flanking sequence oligonucleotide #8.
XX
XX KW Non-identical recognition sequence mutant; sequence-specific recombinase;
XX recombination; antibiotic-resistance marker; loxP; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX PN DE10140030-C1.
XX
XX PD 19-DEC-2002.
XX
XX PF 16-AUG-2001; 2001DE-01040030.
XX
XX PR 16-AUG-2001; 2001DE-01040030.
XX
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX
XX PI Altmann M, Neuhierl B, Hammerschmidt W;
XX
XX DR WPI; 2003-048025/05.
XX
XX PT Method for performing multiple recombination events in a genetic system,
XX useful e.g. for removing antibiotic resistance genes, uses mutant
XX recombination sites.
XX
XX PS Claim 3; Col 9; 10pp; German.
XX
XX CC The present invention relates to the use of two non-identical recognition
XX sequence mutants for a sequence-specific recombinase for performing two
XX or more recombination events, mediated by the sequence-specific
XX recombinase, in a single genetic system. The method is used to manipulate
XX genetic systems (microbial, plant or animal) by site-specific
XX recombination, e.g. to insert or remove DNA and most particularly to
XX remove antibiotic-resistance markers. The present sequence was used to
XX isolate the loxP coding sequence in the exemplification of the invention
XX
XX SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 34; DB 8; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 0.0002;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
XX
XX DB 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
XX
XX RESULT 6
XX ABZ79444
XX ID ABZ79444 standard; DNA; 34 BP.
XX
XX AC ABZ79444;
XX
XX XX DT 23-MAY-2003 (first entry)
XX
XX DE Lox 71 DNA # SEQ ID 1.
XX
XX KW LoxP; lox 71; knockout mouse; vascularisation; embryonic stem cell;
XX drug development; locus of crossing over; ds.
XX
XX OS Synthetic.
XX
XX PN JP2002369689-A.
XX
XX PD 24-DEC-2002.
XX
XX PF 25-MAY-2001; 2001JP-00157568.
XX
XX PR 25-MAY-2001; 2001JP-00157568.
XX
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX (IDEH/) IDE H.
XX PA (YAMA/) YAMAMURA K.
XX PA (ARAK/) ARAKI Y.
XX
XX DR WPI; 2003-125824/12.
XX
XX PT Knockout mouse or embryonic stem cells with introduced trap vectors
XX containing a loxP sequence or a variant loxP sequence with disrupted gene
XX of sequence No. 7 of 1405 bases.

```

XX Claim 4; Fig 4; 21pp; Japanese.

XX The invention relates to a knockout mouse or embryonic stem cells with

XX introduced trap vectors containing a loxP sequence. The knockout animals

CC of the invention may be used in the analysis of genomic functions,

CC particularly for investigating the processes of vascularisation and the

CC development of drugs participating in such processes. The current

CC sequence represents lox 71

XX

SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 8; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 7

ACC85309

ID ACC85309 standard; DNA; 34 BP.

XX

AC ACC85309;

XX

DT 18-SEP-2003 (first entry)

XX

DE Recombinase lox71 DNA recognition sequence.

XX

KW Vegetable plasmid transformation; transgenic; recognition sequence;

KW plant; site-specific integration; nutrition; seed production;

KW chemical production; ds.

XX

OS Unidentified.

XX

XX WO2003054201-A1.

PN

PD 03-JUL-2003.

XX

XX 16-DEC-2002; 2002WO-EP014303.

PF

XX 20-DEC-2001; 2001DE-01063159.

PR

XX (SUNG-) SUNGENE GMBH & CO KGAA.

PA

XX Biesgen C;

PI

XX WPI; 2003-541820/51.

DR

XX Site-specific integration of DNA into plasmid DNA, useful for making

PT transgenic plants used e.g. as food, by recombinase-mediated insertion.

PT

XX Disclosure; Page 35; 164pp; German.

PS

XX The present invention relates to a method for the site-specific

CC integration of a DNA sequence into the plasmid DNA of a plant or its

CC derived cells. Transgenic plants in which a DNA sequence has been

CC integrated, also their cell cultures, organs, tissues etc. are useful in

CC human or animal nutrition, to produce seeds, and to produce

CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,

CC flavonoids and aromatic agents, dyes, antibodies and vaccines. The

CC present sequence is a recognition sequence shown in the exemplification

CC of the invention

XX

SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 9; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 8

ADD13802/c

ID ADD13802 standard; DNA; 34 BP.

XX

AC ADD13802;

XX

DT 01-JAN-2004 (first entry)

XX

DE Oligonucleotide lox71 DNA.

XX

KW library; transfection; humanized monoclonal antibody; antigen;

KW T cell receptor; primer; ss.

XX

OS Synthetic.

XX

XX EP1298207-A1.

PN

PD 02-APR-2003.

XX

PF 01-OCT-2001; 2001EP-00123596.

PR

XX 01-OCT-2001; 2001EP-00123596.

PR

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PA

XX Breitling F, Moldenhauer G, Poustka A, Kuehlwein T;

PI

XX WPI; 2003-383833/37.

DR

XX Preparing library of protein-producing eukaryotic cells, useful for

PT producing humanized high-affinity antibodies, comprises introducing

PT specific recombination signals into chromosomal gene loci and integrating

PT a variety of DNA sequences.

XX

XX Example 7; Page 15; 75pp; German.

PS

XX This invention describes a novel method of preparing a library of protein

CC -producing eukaryotic cells comprising (a) introducing specific

CC recombination signals into one or two chromosomal gene loci, (b)

CC expanding at least one of the modified cells, (c) Transfecting many

CC different DNA sequences, each flanked by recombination signals, into the

CC expanded cells and (d) integrating the DNA sequences into the gene loci

CC on the basis of the recombination signals and the appropriate

CC recombinase. The resulting cells express different proteins, each from an

CC integrated DNA sequence and the proteins are bound to the cell surface.

CC The method is particularly used to produce libraries of humanized

CC monoclonal antibodies, for selection of those with affinity for

CC particular antigens and useful for diagnostic or therapeutic use.

CC Libraries of T cell receptors may also be prepared. The method produces

CC libraries of high diversity; provides easy, quick and automatable

CC selection from a large number of proteins, allows relatively simple

CC alteration of the expressed gene (e.g. fusion to other protein-coding

CC sequences), is suitable for large scale protein production and allows

CC simple verification and characterization of selected cell lines. The

CC method does not require incorporation of a resistance marker. This

CC sequence represents oligonucleotide lox71.

XX

SQ Sequence 34 BP; 12 A; 5 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 9

ADD15151
 ID ADD15151 standard; DNA; 34 BP.
 XX
 AC ADD15151;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Variant loxP DNA recombination site designated lox71 (SeqID 3).
 XX
 KW loxP site; circular; transgenic; plant; non-replicating; transgene;
 KW growth regulant; insect resistance; fungal disease resistance;
 KW stress resistance; ss; lox71.
 XX
 OS Unidentified.
 XX
 PN US2003100077-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 20-SEP-2001; 2001US-00957660.
 XX
 PR 20-SEP-2001; 2001US-00957660.
 XX
 PA (KORT/) KORTE J A.
 PA (LOWE/) LOWE B A.
 XX
 PI Korte JA, Lowe BA;
 XX
 DR WPI; 2003-777313/73.
 XX
 PT Preparing a non-replicating, circular nucleic acid molecule useful for
 PT transforming crop plants to add desirable trait such as herbicide
 PT resistance, by amplifying starting circular nucleic acid molecule.
 XX
 PS Claim 11; SEQ ID NO 3; 66pp; English.
 XX
 CC This invention relates to an in vitro method to create circular molecules
 CC for use in transformation for the generation of transgenic plants.
 CC Specifically, it refers to a preparing a non-replicating, circular
 CC nucleic acid molecule using a first non-mutagenizing oligonucleotide
 CC primer with a nucleic acid sequence complementary to a selected sequence
 CC of the starting circular DNA molecule. As such, the present invention
 CC describes a method useful for preparing a fertile transgenic plant
 CC derived from a dicotyledonous plant preferably soybean and the transgenic
 CC cell is from a monocotyledon, preferably maize. The transgene can be a
 CC plant growth regulant with a selectable phenotype that confers an
 CC advantageous trait, for example, insect resistance, bacterial or fungal
 CC disease resistance, enhanced nutrient utilisation or stress resistance.
 CC This oligonucleotide sequence is a variant of the wild type loxP DNA
 CC recombination site known as lox71, used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 34; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 XX
 RESULT 10
 ABZ75319
 ID ABZ75319 standard; DNA; 34 BP.
 XX
 AC ABZ75319;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE Lox71 related sequence.
 XX
 PT

KW Lox71; knockout animal; Tubedown-1; genomic function analysis;
 KW organ development; ds.
 XX
 OS Unidentified.
 XX
 PN JP2002345477-A.
 XX
 PD 03-DEC-2002.
 XX
 PF 25-MAY-2001; 2001JP-00157567.
 XX
 PR 25-MAY-2001; 2001JP-00157567.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (IDEH/) IDE H.
 PA (YAMA/) YAMAMURA K.
 PA (ARAK/) ARAKI Y.
 XX
 DR WPI; 2003-072475/07.
 XX
 PT Knockout animals with introduced a trap vector containing a variant loxP
 PT with introduced variation in a part of sequence(s) of a spacer sequence,
 PT and reverse repetitive sequence 1 and/or 2.
 XX
 PS Claim 3; Page 12; 22pp; Japanese.
 XX
 CC The invention relates to novel knockout animals with the disrupted
 CC Tubedown-1 gene. The transgenic animals of the invention are useful for
 CC analysis of genomic functions, and establishment of an analytic system
 CC for the development of organs. The present sequence is related to Lox71
 XX
 SQ Sequence 34 BP; 11 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 34; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 XX
 RESULT 11
 ABZ20936
 ID ABZ20936 standard; DNA; 44 BP.
 XX
 AC ABZ20936;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Lox71 isolation oligonucleotide.
 XX
 KW Non-identical recognition sequence mutant; sequence-specific recombinase;
 KW recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
 XX
 OS Unidentified.
 XX
 PN DE10140030-C1.
 XX
 PD 19-DEC-2002.
 XX
 PF 16-AUG-2001; 2001DE-01040030.
 XX
 PR 16-AUG-2001; 2001DE-01040030.
 XX
 PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
 XX
 PI Altmann M, Neuhiel B, Hammerschmidt W;
 XX
 DR WPI; 2003-048025/05.
 XX
 PT Method for performing multiple recombination events in a genetic system,

PT useful e.g. for removing antibiotic resistance genes, uses mutant
 PT recombinease recognition sites.
 XX
 PS Example; Fig 1; 10pp; German.
 XX

CC The present invention relates to the use of two non-identical recognition
 CC sequence mutants for a sequence-specific recombinease for performing two
 CC or more recombination events, mediated by the sequence-specific
 CC recombinease, in a single genetic system. The method is used to manipulate
 CC genetic systems (microbial, plant or animal) by site-specific
 CC recombination, e.g. to insert or remove DNA and most particularly to
 CC remove antibiotic-resistance markers. The present sequence was used to
 CC isolate the lox66 and lox71 coding sequences in the exemplification of
 CC the invention
 XX

SQ Sequence 44 BP; 11 A; 10 C; 6 G; 17 T; 0 U; 0 Other;
 Query Match 100.0%; Score 34; DB 8; Length 44;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 |||||
 DB 6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39
 |||||

RESULT 12
 ABZ20922
 ID ABZ20922 standard; DNA; 68 BP.
 AC ABZ20922;
 XX
 DT 10-APR-2003 (first entry)
 XX

DE Lox66 and lox71 isolation oligonucleotide #1.
 XX

KW Non-identical recognition sequence mutant; sequence-specific recombinease;
 KW recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
 KW ss.
 XX

OS Unidentified.
 XX

XX DE10140030-C1.
 XX

PD 19-DEC-2002.
 XX

PF 16-AUG-2001; 2001DE-01040030.
 XX

PR 16-AUG-2001; 2001DE-01040030.
 XX

XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
 XX

PI Altmann M, Neuhierl B, Hammerschmidt W;
 XX

DR WPI; 2003-048025/05.
 XX

PT Method for performing multiple recombination events in a genetic system,
 PT useful e.g. for removing antibiotic resistance genes, uses mutant
 PT recombinease recognition sites.
 XX

PS Example; Col 6; 10pp; German.
 XX

CC The present invention relates to the use of two non-identical recognition
 CC sequence mutants for a sequence-specific recombinease for performing two
 CC or more recombination events, mediated by the sequence-specific
 CC recombinease, in a single genetic system. The method is used to manipulate
 CC genetic systems (microbial, plant or animal) by site-specific
 CC recombination, e.g. to insert or remove DNA and most particularly to
 CC remove antibiotic-resistance markers. The present sequence was used to
 CC isolate the lox66 and lox71 coding sequences in the exemplification of
 CC the invention
 XX

SQ Sequence 68 BP; 16 A; 16 C; 14 G; 22 T; 0 U; 0 Other;
 Query Match 100.0%; Score 34; DB 5; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.00021;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 34; DB 8; Length 68;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
 |||||
 DB 11 TACCGTTCGTATAGCATACATTATACGAAGTTAT 44
 |||||

RESULT 13
 AAD04925/c
 ID AAD04925 standard; DNA; 78 BP.
 XX
 AC AAD04925;
 XX

DT 17-JUL-2001 (first entry)
 XX

DE Primer lox3 for synthesising DNA fragment with loxP mutant sites.
 XX

KW Gene trapping construct; conditional mutation; unidirectional inversion;
 KW recombinease recognition sequence; RRS; disruption cassette;
 KW selection cassette; transgenic organism; loxP site; primer; ss.
 XX

OS Enterobacteria phage P1.
 OS Synthetic.
 XX

PN WO200129208-A1.
 XX

PD 26-APR-2001.
 XX

PF 16-OCT-2000; 2000WO-EP010162.
 XX

PR 16-OCT-1999; 99EP-00120592.
 PR 27-OCT-1999; 99US-0162016P.
 XX

XX (ARTE-) ARTEMIS PHARM GMBH.
 PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
 XX

PI Kuehn R, Von Melchener H, Altschmied J;
 XX

DR WPI; 2001-308486/32.
 XX

PT New gene trapping construct capable of causing conditional mutations in
 PT genes, comprises functional DNA segment inserted in sense or antisense
 PT direction relative to gene to be trapped.
 XX

PS Example 1; Page 18; 78pp; English.
 XX

CC The present invention relates to a conditional gene trapping construct
 CC capable of causing conditional mutations in genes. The gene trapping
 CC construct comprises two functional DNA segments, each being flanked by
 CC two recombinease recognition sequences (RRSs) specific to site specific
 CC recombinease which is capable of unidirectional inversion of double
 CC standard DNA segment. One of the DNA segment (disruption cassette) is
 CC inserted in antisense orientation relative to the transcriptional
 CC orientation of the gene to be trapped. The other DNA segment (selection
 CC cassette) is inserted in sense direction relative to the transcriptional
 CC orientation of the gene to be trapped. The cell comprising the gene
 CC trapping construct is useful for the identification and/or isolation of
 CC genes. The transgenic organism comprising the gene trapping construct is
 CC useful to study gene function at various developmental stages. The gene
 CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present sequence is a primer lox3 which is used for
 CC synthesising a DNA fragment containing a lox66 and a lox71 Cre
 CC recombinease recognition mutant sites in opposite orientation. The primer
 CC is used for constructing the gene trap vector pRK57SA-beta
 XX

SQ Sequence 78 BP; 27 A; 14 C; 14 G; 23 T; 0 U; 0 Other;
 Query Match 100.0%; Score 34; DB 5; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.00021;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 78 TACCGTTCGTATAGCATACATTATACGAAGTTAT 45

RESULT 14
AAD04926
ID AAD04926 standard; DNA; 79 BP.
XX
AC AAD04926;
XX
DT 17-JUL-2001 (first entry)
XX
DE Primer lox4 for synthesising DNA fragment with loxP mutant sites.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; primer; ss.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOLOGIE AG.
XX
PI Kuehn R, Von Melchener H, Altschmied J;
XX
DR WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Example 1; Page 18-19; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific
CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene
CC trapping construct is useful for mutationally inactivating all cellular
CC genes. The present sequence is a primer lox4 which is used for
CC synthesising a DNA fragment containing a lox66 and a lox71 Cre
CC recombinase recognition mutant sites in opposite orientation. The primer
CC is used for constructing the gene trap vector pRK57SA-beta
XX
SQ Sequence 79 BP; 24 A; 14 C; 14 G; 27 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 5; Length 79;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39

RESULT 15
ABV75994
ID ABV75994 standard; DNA; 94 BP.
XX
AC ABV75994;
XX
DT 11-FEB-2003 (first entry)
XX
DE OLIGO-F, contains attP and attB sites for phage phi-C31 integrase.
XX
KW AttP; attB; phage phi-C31; integrase; recombination; minicircle;
KW gene therapy; mitochondria; ss.
XX
OS Bacteriophage phi-C31.
OS Synthetic.
XX
PN WO200283889-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-GB001668.
XX
PR 10-APR-2001; 2001GB-00008968.
PR 05-OCT-2001; 2001US-0327029P.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Bigger BW, Tolmachov O, Coutelle C;
XX
DR WPI; 2003-075546/07.
XX
PT New cell capable of expressing an endonuclease, useful for producing a
PT minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT capable of recombination to form a minicircle and a miniplasmid.
XX
PS Example 3; Page 46; 70pp; English.
XX
CC The present sequence is that of oligonucleotide OLIGO-F, which was
CC annealed to OLIGO-R (see ABV75994) and introduced into plasmid pBC-SK(+),
CC thereby creating attP and attB recombination sites. Minicircle-producing
CC plasmids with attP and attB sites for phage phi-C31 integrase were
CC constructed. This is an example of a method of the invention for the
CC production of a minicircle. In this method, a plasmid having a DNA
CC sequence flanked by attP and attB sites is exposed to phi-C31 integrase,
CC thereby forming a minicircle comprising the DNA sequence and a
CC miniplasmid comprising the remainder of the plasmid. The minicircle is
CC useful for mitochondrial gene therapy
XX
SQ Sequence 94 BP; 33 A; 19 C; 15 G; 27 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 8; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83

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Job time : 203.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 19:07:03 ; Search time 69 Seconds
(without alignments)
806.281 Million cell updates/sec

Title: US-10-030-658B-15
Perfect score: 34
Sequence: 1 taccgttcgtatgacatacattacgaagtat 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	29	85.3	34	1	US-08-214-023-1
C 2	29	85.3	34	1	US-08-214-023-2
C 3	29	85.3	34	1	US-08-615-048-1
C 4	29	85.3	34	2	US-08-864-224-12
C 5	29	85.3	34	2	US-08-743-796-1
C 6	29	85.3	34	2	US-08-350-260A-1
C 7	29	85.3	34	2	US-08-350-260A-601
C 8	29	85.3	34	3	US-08-654-623-4
C 9	29	85.3	34	3	US-09-011-257-1
C 10	29	85.3	34	3	US-08-412-777-1
C 11	29	85.3	34	3	US-08-412-826-1
C 12	29	85.3	34	3	US-09-214-471-1
C 13	29	85.3	34	3	US-09-193-475-1
C 14	29	85.3	34	3	US-09-563-239-1
C 15	29	85.3	34	3	US-09-271-055A-1
C 16	29	85.3	34	3	US-09-603-663-1
C 17	29	85.3	34	3	US-09-603-663-5
C 18	29	85.3	34	3	US-09-603-658-1
C 19	29	85.3	34	3	US-09-603-658-5
C 20	29	85.3	34	3	US-09-602-373A-1
C 21	29	85.3	34	3	US-09-602-373A-5
C 22	29	85.3	34	3	US-09-661-364-1
C 23	29	85.3	34	3	US-09-610-259-1
C 24	29	85.3	34	3	US-09-554-271A-1
C 25	29	85.3	34	3	US-09-837-863-1
C 26	29	85.3	34	4	US-09-104-337A-1
C 27	29	85.3	34	4	US-09-293-303-1
C 28	29	85.3	34	4	US-09-718-034-2
C 29	29	85.3	34	4	US-09-606-323C-1
C 30	29	85.3	34	4	US-09-703-399A-1
C 31	29	85.3	34	4	US-09-703-399A-5
C 32	29	85.3	34	4	US-09-377-885A-1
C 33	29	85.3	34	4	US-09-377-885A-20
C 34	29	85.3	34	4	US-09-975-304-1
C 35	29	85.3	34	4	US-09-411-826-1
C 36	29	85.3	34	4	US-10-072-047-1
C 37	29	85.3	34	4	US-09-662-128A-3
C 38	29	85.3	34	4	US-09-856-110B-1
C 39	29	85.3	34	4	US-09-856-110B-2
C 40	29	85.3	34	4	US-09-937-837-5
C 41	29	85.3	34	4	US-09-829-507-1
C 42	29	85.3	34	4	US-09-122-384-12
C 43	29	85.3	34	4	US-09-329-582A-1
C 44	29	85.3	34	5	PCT-US93-00108-1
C 45	29	85.3	34	5	PCT-US93-00108-2

RESULT 1
US-08-214-023-1/c
; Sequence 1, Application US/08214023
; Patent No. 5434066
; GENERAL INFORMATION:
; APPLICANT: BEBER, ROBERT L
; APPLICANT: HARTLEY, JAMES L
; TITLE OF INVENTION: MODULATION OF ENZYME ACTIVITIES IN THE
; TITLE OF INVENTION: IN VIVO CLONING OF DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEIL, GOTSHAL & MANGES
; STREET: 1615 L STREET, N.W.; SUITE 700
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,023
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 59452.0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 682-7033
; TELEFAX: (202) 859-0939
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: ESCHERICHIA COLI
; STRAIN: DH10B
; US-08-214-023-1

ALIGNMENTS

Query Match 85.3%; Score 29; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTCGTATAGCATACATTATACGAAGTTAT 34
 Db 29 TTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 2

US-08-214-023-2
 ; Sequence 2, Application US/08214023
 ; Patent No. 5434066
 ; GENERAL INFORMATION:
 ; APPLICANT: BEBEE, ROBERT L
 ; APPLICANT: HARTLEY, JAMES L
 ; TITLE OF INVENTION: MODULATION OF ENZYME ACTIVITIES IN THE
 ; TITLE OF INVENTION: IN VIVO CLONING OF DNA
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WEILL, GOTSHAL & MANGES
 ; STREET: 1615 L STREET, N.W.; SUITE 700
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20036

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/214,023
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/862,188
 ; FILING DATE:

ATTORNEY/AGENT INFORMATION:
 ; NAME: AUERBACH, JEFFREY I
 ; REGISTRATION NUMBER: 32,680
 ; REFERENCE/DOCKET NUMBER: 59452.0011
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 682-7033
 ; TELEFAX: (202) 859-0939
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: ESCHERICHIA COLI
 ; STRAIN: DH10B
 ; US-08-214-023-2

Query Match 85.3%; Score 29; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTCGTATAGCATACATTATACGAAGTTAT 34
 Db 6 TTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 3

US-08-615-048-1
 ; Sequence 1, Application US/08615048
 ; Patent No. 5700470
 ; GENERAL INFORMATION:

APPLICANT: Saito, Izumu
 APPLICANT: Kanegae, Yumi
 APPLICANT: Nakai, Michio
 TITLE OF INVENTION: RECOMBINANT DNA VIRUS AND METHOD FOR
 TITLE OF INVENTION: PREPARATION THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 STREET: 2100 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20037

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/615,048
 ; FILING DATE: 12-MAR-1996
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:

NAME: Nakamura, Dean H.
 REGISTRATION NUMBER: 33,981
 REFERENCE/DOCKET NUMBER: Q-41057
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)293-7060
 ; TELEFAX: (202)293-7860
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-615-048-1

Query Match 85.3%; Score 29; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTCGTATAGCATACATTATACGAAGTTAT 34
 Db 6 TTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 4

US-08-864-224-12
 ; Sequence 12, Application US/08864224
 ; Patent No. 5851808
 ; GENERAL INFORMATION:
 ; APPLICANT: Ellledge, Stephen J.
 ; APPLICANT: Liu, Qinghua
 ; TITLE OF INVENTION: Rapid Subcloning Using Site-Specific
 ; TITLE OF INVENTION: Recombination
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Medlen & Carroll, LLP
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94104

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/864,224
 ; FILING DATE:
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: BCM-02681
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 US-08-864-224-12

Query Match 85.3%; Score 29; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
 Db 6 TTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 5
 US-08-743-796-1/c
 Sequence 1, Application US/08743796
 Patent No. 5928914
 GENERAL INFORMATION:
 APPLICANT: Leboultch, P. et al.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
 OPERATING SYSTEM: TRANSFORMING CELLS
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/743,796
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane E. Remillard
 REGISTRATION NUMBER: 38,872
 REFERENCE/DOCKET NUMBER: MTR-198
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-743-796-1

Query Match 85.3%; Score 29; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
 Db 29 TTCGTATAGCATACATTATACGAAGTTAT 1
 RESULT 6
 US-08-350-260A-1/c
 Sequence 1, Application US/08350260A
 Patent No. 5962255
 GENERAL INFORMATION:
 APPLICANT: Winter, Gregory Paul
 APPLICANT: Griffiths, Andrew David
 APPLICANT: Williams, Samuel Cameron
 APPLICANT: Waterhouse, Peter
 APPLICANT: Nissim, Anuva
 APPLICANT: Johnson, Kevin Stuart
 APPLICANT: Smith, Andrew John Hammond
 TITLE OF INVENTION: Methods for producing members of specific
 TITLE OF INVENTION: binding pairs
 NUMBER OF SEQUENCES: 602
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David W. Clough
 STREET: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/350,260A
 FILING DATE: 05-DEC-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9110549.4
 FILING DATE: 15-MAY-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB91/01134
 FILING DATE: 10-JUL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/00883
 FILING DATE: 15-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB93/00605
 FILING DATE: 24-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/150,002
 FILING DATE: 31-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/307,619
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Clough, David W
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 28111/32372
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 US-08-350-260A-1

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-350-260A-601
0; Gaps 0; Indels 0; Mismatches 0;

Query Match      85.3%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db      29 TTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 7
US-08-350-260A-601/c
; Sequence 601, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-350-260A-601
0; Gaps 0; Indels 0; Mismatches 0;

Query Match      85.3%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTCGTATAGCATACATTATACGAAGTTAT 34
      |||||
Db      29 TTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 8
US-08-654-623-4/c
; Sequence 4, Application US/08654623
; Patent No. 6010884
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Holliger, Kaspar-Philipp
; APPLICANT: Nissim, Ahuva
; APPLICANT: Fisch, Igor
; APPLICANT: Winter, Gregory P
; TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/654,623
; FILING DATE: 29-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225453.1
; FILING DATE: 04-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9300816.7
; FILING DATE: 16-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93303614.7
; FILING DATE: 10-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9319969.3
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02492
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9412147.2
; FILING DATE: 17-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02662
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,418
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; INFORMATION FOR SEQ ID NO: 4:
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SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: Other nucleic acid: plasmid DNA
 US-08-654-623-4

Query Match 85.3%; Score 29; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATACATACATATACGAAGTTAT 34
 |||||
 DB 29 TTCGTATACATACATATACGAAGTTAT 1

RESULT 9

US-09-011-257-1/c
 ; Sequence 1, Application US/09011257
 ; Patent No. 6086478
 ; GENERAL INFORMATION:
 ; APPLICANT: LUSKY, Monika
 ; APPLICANT: MEHTALI, Majid
 ; TITLE OF INVENTION: HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS
 ; FILE REFERENCE: 017753-090
 ; CURRENT APPLICATION NUMBER: US/09/011,257
 ; EARLIER FILING DATE: 1998-03-09
 ; EARLIER FILING DATE: FR 95/09.289
 ; EARLIER FILING DATE: 1995-07-31
 ; EARLIER APPLICATION NUMBER: PCT/FR96/01200
 ; EARLIER FILING DATE: 1996-07-30
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 34
 ; TYPE: DNA
 ; ORGANISM: Bacteriophage P1
 US-09-011-257-1

Query Match 85.3%; Score 29; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATACATACATATACGAAGTTAT 34
 |||||
 DB 29 TTCGTATACATACATATACGAAGTTAT 1

RESULT 10

US-08-412-777-1/c
 ; Sequence 1, Application US/08412777
 ; Patent No. 6091001
 ; GENERAL INFORMATION:
 ; APPLICANT: JAKOBOVITS, AYA
 ; APPLICANT: ZSEBO, KRISTINA M.
 ; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES USING
 ; CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CELL GENESYS, INC.
 ; STREET: 322 LAKESIDE DRIVE
 ; CITY: FOSTER CITY
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES
 ; ZIP: 94404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 29-MAR-1995
 ; APPLICATION NUMBER: US/08/412,777

FILING DATE: 29-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MANDEL, SARALYNN
 REGISTRATION NUMBER: 31,853
 REFERENCE/DOCKET NUMBER: CELL20
 TELEPHONE: (415)358-9600 X345
 TELEFAX: (415)349-7392
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-412-777-1

Query Match 85.3%; Score 29; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATACATACATATACGAAGTTAT 34
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 DB 29 TTCGTATACATACATATACGAAGTTAT 1

RESULT 11

US-08-412-826-1/c
 ; Sequence 1, Application US/08412826
 ; Patent No. 6130364
 ; GENERAL INFORMATION:
 ; APPLICANT: JAKOBOVITS, AYA
 ; APPLICANT: ZSEBO, KRISTINA M.
 ; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES USING
 ; CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CELL GENESYS, INC.
 ; STREET: 322 LAKESIDE DRIVE
 ; CITY: FOSTER CITY
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES
 ; ZIP: 94404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 29-MAR-1995
 ; APPLICATION NUMBER: US/08/412,826
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MANDEL, SARALYNN
 ; REGISTRATION NUMBER: 31,853
 ; REFERENCE/DOCKET NUMBER: CELL21
 ; TELEPHONE: (415)358-9600 X345
 ; TELEFAX: (415)349-7392
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-412-826-1

Query Match 85.3%; Score 29; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.0013;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
|||||
Db 29 TTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 12

US-09-214-471-1
; Sequence 1, Application US/09214471
; Patent No. 6201186
; GENERAL INFORMATION:
; APPLICANT: Kohara, Michinori
; APPLICANT: Wakita, Takaji
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Saito, Izumu
; TITLE OF INVENTION: Hepatitis C Animal Model
; FILE REFERENCE: sequence listing 382.1025
; CURRENT APPLICATION NUMBER: US/09/214,471
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: PCT/JP97/02575
; EARLIER FILING DATE: 1997-07-24
; EARLIER APPLICATION NUMBER: 195076/1996 JAPAN
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: E. coli p1 phage
US-09-214-471-1

Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db 6 TTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 13

US-09-193-475-1
; Sequence 1, Application US/09193475
; Patent No. 6300545
; GENERAL INFORMATION:
; APPLICANT: Baszczynski, Christopher L.
; APPLICANT: Lyznik, Leszek
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Guan, Xueni
; TITLE OF INVENTION: Mobilization of Viral Genomes From T-DNA
; FILE REFERENCE: 5718-61
; CURRENT APPLICATION NUMBER: US/09/193,475
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/099,461
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: 60/065,627
; EARLIER FILING DATE: 1997-11-18
; EARLIER APPLICATION NUMBER: 60/065,613
; EARLIER FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: wild type loxP recombination site
US-09-193-475-1

Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
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Db 6 TTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 14

US-09-563-239-1/c
; Sequence 1, Application US/09563239
; Patent No. 6350575
; GENERAL INFORMATION:
; APPLICANT: LUSKY, Monika
; APPLICANT: MEHTALI, Majid
; TITLE OF INVENTION: HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS
; FILE REFERENCE: 017753-090
; CURRENT APPLICATION NUMBER: US/09/563,239
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/011,257
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/FR96/01200
; PRIOR FILING DATE: 1996-07-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Bacteriophage P1
US-09-563-239-1

Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
|||||
Db 29 TTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 15

US-09-271-055A-1/c
; Sequence 1, Application US/09271055A
; Patent No. 6406847
; GENERAL INFORMATION:
; APPLICANT: David Cox
; APPLICANT: Malek Fahan
; APPLICANT: Siamak Baharloo
; TITLE OF INVENTION: Mismatch Repair Detection
; FILE REFERENCE: UCSF-127CIP
; CURRENT APPLICATION NUMBER: US/09/271,055A
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 08/713,751
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: 60/004,664
; PRIOR FILING DATE: 1995-10-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: lambda phage
US-09-271-055A-1

Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TTCGTATAGCATACATTATACGAAGTTAT 34
|||||
Db 29 TTCGTATAGCATACATTATACGAAGTTAT 1

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Job time : 71 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-030-658B-15

Perfect score: 34
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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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23: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
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25: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:
26: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	10	US-09-957-660-3
2	34	100.0	34	14	US-10-214-722-6
3	34	100.0	34	14	US-10-214-722-8
4	34	100.0	34	18	US-10-416-985-9
5	34	100.0	34	19	US-10-739-769-3
6	34	100.0	34	20	US-10-448-395-2
7	34	100.0	34	20	US-10-448-395-13

ALIGNMENTS

RESULT 1

US-09-957-660-3

; Sequence 3, Application US/09957660

; Publication No. US20030100077A1

; GENERAL INFORMATION:

; APPLICANT: KORTE, JOHN A.

; APPLICANT: LOWE, BRENDA A.

; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN

; TITLE OF INVENTION: TRANSFORMATION

; FILE REFERENCE: DEPM:176US

; CURRENT APPLICATION NUMBER: US/09/957,660

; CURRENT FILING DATE: 2001-09-20

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 34

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Primer

US-09-957-660-3

Query Match 100.0%; Score 34; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.00057;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATTATACGAAGTTAT 34

Db 1 TACCGTTCGTATAGCATTATACGAAGTTAT 34

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Sequence 16, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 16, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 1, Appl
Sequence 3, Appl
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Sequence 1, Appl
Sequence 20, Appl
Sequence 6, Appl
Sequence 29, Appl
Sequence 7, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 52, Appl
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Sequence 1, Appl
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Sequence 4, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 1, Appl
Sequence 5, Appl

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RESULT 2
US-10-214-722-6
; Sequence 6, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombinase-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 71 without flanks
US-10-214-722-6
Query Match 100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 3
US-10-214-722-8
; Sequence 8, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombinase-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-8
Query Match 100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 4
US-10-416-995-9/c
; Sequence 9, Application US/10416995
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; Publication No. US20040077089A1
; GENERAL INFORMATION:
; APPLICANT: Xin, Hong-Bo
; APPLICANT: Koclikoff, Michael
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: VECTORS FOR CONDITIONAL GENE INACTIVATION
; FILE REFERENCE: 1153.020US1
; CURRENT APPLICATION NUMBER: US/10/416,995
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCI/US01/43916
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,200
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: A mutant loxP sequence
US-10-416-995-9
Query Match 100.0%; Score 34; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 5
US-10-739-769-3
; Sequence 3, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Methods of Site-Directed Transformation
; FILE REFERENCE: 38-15(52823)B
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild-type loxP recombination site
US-10-739-769-3
Query Match 100.0%; Score 34; DB 19; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

RESULT 6
US-10-448-395-2/c
; Sequence 2, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
```

/ ; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-2

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||
Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 7
US-10-448-395-13/c
; Sequence 13, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-13

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||
Db 34 TACCGTTCGTATAGCATACATTATACGAAGTTAT 1

RESULT 8
US-10-448-395-15
; Sequence 15, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide

US-10-448-395-15

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||
Db 6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39

RESULT 9

US-10-448-395-16/c
; Sequence 16, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-16

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||
Db 39 TACCGTTCGTATAGCATACATTATACGAAGTTAT 6

RESULT 10

US-10-214-722-15
; Sequence 15, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; FILE REFERENCE: P14567
; CURRENT FILING DATE: 2002-08-07
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 15
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 71 with flanks
US-10-214-722-15

Query Match 100.0%; Score 34; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00059;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34

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Db      6 TACCGTTCGTATAGCATACATTATACGAAGTTAT 39
|||||
RESULT 11
US-10-214-722-11
; Sequence 11, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; FILE OF INVENTION: consecutive recombinase-mediated recombination
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-11
Query Match      100.0%; Score 34; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||||

Db      11 TACCGTTCGTATAGCATACATTATACGAAGTTAT 44
|||||

RESULT 12
US-10-118-231-10
; Sequence 10, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-118-231-10
Query Match      100.0%; Score 34; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db      50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83
|||||

RESULT 13
US-10-118-231-16
; Sequence 16, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-118-231-16
Query Match      100.0%; Score 34; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
|||||

Db      50 TACCGTTCGTATAGCATACATTATACGAAGTTAT 83
|||||

RESULT 14
US-10-448-395-1/C
; Sequence 1, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-1
Query Match      100.0%; Score 34; DB 20; Length 2133;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db      153 TACCGTTCGTATAGCATACATTATACGAAGTTAT 120
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RESULT 15
US-10-214-722-7
; Sequence 7, Application US/10214722
; Publication No. US20030082723A1
```

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; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombination-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-7

Query Match      95.3%; Score 32.4; DB 14; Length 34;
Best Local Similarity 97.1%; Pred. No. 0.0025;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db      1 TAGCGTTCGTATAGCATACATTATACGAAGTTAT 34

Search completed: September 8, 2005, 23:04:39
Job time : 310 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	32.4	95.3	422	7	CF978723	2-33-C10.
C 2	30.8	90.6	449	2	BF133141	BF133141 601645577
3	30.8	90.6	575	7	CF975530	CF975530 2-97-F02.
4	30.8	90.6	670	7	CF977704	CF977704 2-97-H02.
C 5	30.8	90.6	696	7	CF974915	CF974915 2-2-E01.R
C 6	30.8	90.6	739	8	AQ864471	AQ864471 nbe50023G
C 7	30.8	90.6	810	8	AQ865062	AQ865062 nbe50024N
C 8	30.8	90.6	896	2	BE748939	BE748939 601571869
C 9	30.8	90.6	1049	5	CL111198	CL111198 ASBI-54P4
10	30	88.2	889	6	CB198925	CB198925 ASBENCOURT
11	30	88.2	910	7	CN385562	CN385562 LE2TR03P0
12	29.4	86.5	235	7	CF979500	CF979500 2-97-A01.
C 13	29.4	86.5	441	8	AQ869026	AQ869026 nbe50033I
C 14	29.4	86.5	452	8	AQ316088	AQ316088 nbe50061K
C 15	29.4	86.5	633	8	AQ871906	AQ871906 nbe50045C
C 16	29.4	86.5	771	8	AQ864951	AQ864951 nbe50024B
C 17	29.4	86.5	802	8	AQ858133	AQ858133 nbe50012E
C 18	29.4	86.5	826	8	AQ863178	AQ863178 nbe50020B
C 19	29.2	85.9	160	4	BG536159	BG536159 602564263
C 20	29.2	85.9	385	6	CB354804	CB354804 ZF001-P00
C 21	29.2	85.9	443	5	BP626390	BP626390 BP626390
22	29.2	85.9	562	6	CB352860	CB352860 ZF001-P00
C 23	29.2	85.9	849	8	BI19733	BI19733 F23L9-Sp6 I
C 24	29.2	85.9	904	9	CL140878	CL140878 ISB1-118B

Db

17 TACGGTTCGTATAGCATACATTATACGAAGTTAT 50

RESULT 2

BF133141/c
LOCUS
DEFINITION
60164557R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3930715 3', mRNA linear EST 24-OCT-2000

ACCESSION
BF133141
VERSION
BF133141.1 GI:10972181
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM765 row: i column: 20
High quality sequence start: 3
High quality sequence stop: 215
Location/Qualifiers
1..449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3930715"
/tissue type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_59"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgccg); Site_2: SfiI (ggcattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGGCGCGGCGCGCATG-dT(30)BN-3'. (Where B = A, C, G or N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

FEATURES
source
1..449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3930715"
/tissue type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_59"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgccg); Site_2: SfiI (ggcattatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGGCGCGGCGCGCATG-dT(30)BN-3'. (Where B = A, C, G or N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 90.6%; Score 30.8; DB 2; Length 449;
Best Local Similarity 94.1%; Pred. No. 0.025;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TACGGTTCGTATAGCATACATTATACGAAGTTAT 34
||| ||||||||||||||||||||||||||||||||
34 TAACCTTCGTATAGCATACATTATACGAAGTTAT 1

Db

RESULT 3
CF975530
LOCUS
DEFINITION
2-97-F02.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA linear EST 24-JUN-2004

ACCESSION
CF975530
VERSION
CF975530.1 GI:49170988
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

AUTHORS
Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
TITLE
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells
JOURNAL
Unpublished (2003)
COMMENT
Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.

FEATURES
source
1..670
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue type="Retinal Ganglion Cells"
/lab_host="DH10B"

ORIGIN
Query Match 90.6%; Score 30.8; DB 7; Length 575;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
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19 TACACTTCGTATAGCATACATTATACGAAGTTAT 52

Db

RESULT 4
CF977704
LOCUS
DEFINITION
2-97-H02.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA linear EST 24-JUN-2004

ACCESSION
CF977704
VERSION
CF977704.1 GI:49173162
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

AUTHORS
Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
TITLE
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells
JOURNAL
Unpublished (2003)
COMMENT
Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.

FEATURES
source
1..670
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue type="Retinal Ganglion Cells"
/lab host="DH10B"

ORIGIN
Query Match 90.6%; Score 30.8; DB 7; Length 575;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
||| ||||||||||||||||||||||||||||||||
19 TACACTTCGTATAGCATACATTATACGAAGTTAT 52

Db

ORIGIN
Query Match 90.6%; Score 30.8; DB 7; Length 670;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 22 TAACCTTCGTATAGCATACATTATACGAAGTTAT 55

RESULT 5
LOCUS CF974915/c
DEFINITION 2-2-E01.R Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
ACCESSION CF974915
VERSION CF974915.1 GI:49170373
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (Bases 1 to 696)
AUTHORS Farkas, R.H., Qian, J., Goldberg, J.L., Quigley, H.A. and Zack, D.J.
TITLE Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells
JOURNAL Unpublished (2003)
COMMENT Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.

FEATURES
source
1. .696
/location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LTB; Site 1: SfiI; Site 2: SfiI; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA Library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."

ORIGIN
Query Match 90.6%; Score 30.8; DB 7; Length 696;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 485 TAACCTTCGTATAGCATACATTATACGAAGTTAT 452

RESULT 6
LOCUS AQ864471/c
DEFINITION nbe0023G19r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica cultivar-group) genomic clone nbe0023G19r, genomic survey sequence.

ACCESSION AQ864471
VERSION AQ864471.1 GI:6214837
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (Bases 1 to 739)
AUTHORS Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 37
High quality sequence stop: 512.

FEATURES
source
1. .739
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone_lib="nbe0023G19r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACindigo; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN
Query Match 90.6%; Score 30.8; DB 8; Length 739;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TACCGTTCGTATAGCATACATTATACGAAGTTAT 34
Db 441 TAACCTTCGTATAGCATACATTATACGAAGTTAT 408

RESULT 7
LOCUS AQ865062/c
DEFINITION nbe0024N11r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica cultivar-group) genomic clone nbe0024N11r, genomic survey sequence.

ACCESSION AQ865062
VERSION AQ865062.1 GI:6215519

KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 810)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 43
High quality sequence stop: 360.
Location/Qualifiers

FEATURES
source

1. .810
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nb0024N11r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACindigo; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, a Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 8; Length 810;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TACCGTTTCGTATAGCATATATACGAAGTTAT 34
|||||
Db 449 TACCTTTGGTATAGCATATATACGAAGTTAT 416
|||||

RESULT 8
BE748939/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE748939
601571869T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838936 3', mRNA sequence.
BE748939
BE748939.1 GI:10162931
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 896)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMS26 row: i column: 17
High quality sequence start: 20
High quality sequence stop: 268.
Location/Qualifiers

FEATURES
source

1. .896
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3838936"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctctggcc); Site 2: SfiI (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTTCAGGCGGCGGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 896;
Best Local Similarity 94.1%; Pred. No. 0.026;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TACCGTTTCGTATAGCATATATACGAAGTTAT 34
|||||
Db 88 TAACCTTCGTATAGCATATATACGAAGTTAT 55
|||||

RESULT 9
CL111198/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL111198
ISB1-54P4 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-54P4, genomic survey sequence.
CL111198
CL111198.1 GI:40604833
GSS.
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.
1. (bases 1 to 1049)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00

Seq primer: Sp6 ATTTAGGTGACACTATAG
 Class: BAC ends
 High quality sequence start: 116
 High quality sequence stop: 895.

FEATURES

Location/Qualifiers
 1..1049
 /organism="Xenopus tropicalis"
 /mol_type="genomic DNA"
 /db_xref="taxon:8364"
 /clone="ISB1-54P4"
 /clone_lib="ISB1"
 /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"

ORIGIN

Query Match 90.6%; Score 30.8; DB 9; Length 1049;
 Best Local Similarity 94.1%; Pred. No. 0.026;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TACCTTCGTATAGCATACATTATACGAAGTTAT 34
 |||
 DB 937 TAACTTCGTATAGCATACATTATACGAAGTTAT 904

RESULT 10

CB198925
 LOCUS
 DEFINITION AGENCOURT 11212397 NICHX KGC Tad2 Xenopus laevis cDNA clone
 IMAGE:6873929 5', mRNA sequence.

ACCESSION CB198925
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Xenopus laevis (African clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Xenopus.

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

On Feb 4, 2003 this sequence version replaced gi:28229700.

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Drs. Donald Brown and Liqun Cai

cDNA Library Preparation: CLONTECH

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM3106 row: 0 column: 16

High quality sequence stop: 476.

FEATURES

Location/Qualifiers
 1..889
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:6873929"
 /dev_stage="metamorphosis stage 62"
 /clone_lib="NICHX KGC Tad2"

/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
 Site 1: Sfil; Site 2: Sfil; 5' and 3' adaptors were used
 in cloning as follows: 5' adaptor sequence:
 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGCCGACATG-DT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.7 kb
 (range 0.8-3.0 kb). 15/15 colonies contained inserts by
 PCR. This library was enriched for full-length clones and
 was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 88.2%; Score 30; DB 6; Length 889;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTTCGTATAGCATACATTATACGAAGTTAT 34
 |||
 DB 8 GTTCGTATAGCATACATTATACGAAGTTAT 37

RESULT 11

CB198562
 LOCUS
 DEFINITION CN385562 Tomato CL5915 roots under different developmental stages
 Lycopersicon esculentum cDNA clone LE2TR03P06, mRNA sequence.

ACCESSION CN385562
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 910)

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Contact: Kin-Ying, To

Crop Plant Improvement Group

Institute of Bioagricultural Sciences, Academia Sinica

128 Academia Rd. Section 2, Taipei, Taiwan 11529

Tel: 886-2-2653-3161

Fax: 886-2-2561-5600

Email: kyto@gate.sinica.edu.tw

Insert Length: 910 Std Error: 0.00

Plate: 03 row: P column: 06

Seq primer: smart2.

FEATURES

Location/Qualifiers
 1..910
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /cultivar="CL5915"
 /db_xref="taxon:4081"
 /clones="LE2TR03P06"
 /tissue_type="roots"
 /dev_stage="1-, 2-, 3-, and 4- month-old"
 /lab_hosts="E.Coli BM25.8"
 /clone_lib="Tomato CL5915 roots under different
 developmental stages"

/note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained
 from AVRDC. Roots were harvested from plants grown under
 different developmental stages: 1-, 2-, 3-, 4-month-old.
 Equal aliquots of mRNA of different developmental stages
 were mixed and used for cDNA library construction. (Smart
 PCR cDNA Library construction kit, Clontech)"

ORIGIN

Query Match 88.2%; Score 30; DB 7; Length 910;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTTCGTATAGCATACATTATACGAAGTTAT 34
 |||
 DB 757 GTTCGTATAGCATACATTATACGAAGTTAT 786

RESULT 12

CF979500
 LOCUS
 DEFINITION CF979500 235 bp mRNA linear EST 24-JUN-2004
 sequence.
 ACCESSION CF979500
 VERSION

CF979500.1 GI:49174961


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/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="nbeb0061K08r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/notes="Vector: pBACindigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

```

ORIGIN

```

Query Match      86.5%; Score 29.4; DB 8; Length 452;
Best Local Similarity 96.8%; Pred. No. 0.097;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 4 CGTTCGTATAGCATACATTATACGAAGTTAT 34
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Db 427 CCTTCGTATAGCATACATTATACGAAGTTAT 397

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```

RESULT 15
LOCUS   AQ871906/c
DEFINITION
nbeb0045C24r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
cultivar-group) genomic clone nbeb0045C24r, genomic survey
sequence.
ACCESSION
AQ871906
VERSION
AQ871906.1 GI:6222357
KEYWORDS
GSS.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 633)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 30
High quality sequence stop: 466.

```

FEATURES

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1..633
Location/Qualifiers
source
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="genomic DNA"
    /cultivar="Nipponbare"

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/db_xref="taxon:39947"
/clone="nbeb0045C24r"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/notes="Vector: pBACindigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

```

ORIGIN

```

Query Match      86.5%; Score 29.4; DB 8; Length 633;
Best Local Similarity 96.8%; Pred. No. 0.098;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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Qy 4 CGTTCGTATAGCATACATTATACGAAGTTAT 34
    |||||
Db 576 CCTTCGTATAGCATACATTATACGAAGTTAT 546

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Search completed: September 9, 2005, 00:32:13
Job time : 1588.5 secs

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Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	34	100.0	34	6	BD182869	BD182869 Knockout	
2	34	100.0	34	6	BD185623	BD185623 Knockout	
3	34	100.0	34	6	AX114842	AX114842 Sequence	
4	34	100.0	34	6	AX137068	AX137068 Sequence	
5	34	100.0	34	6	AX540641	AX540641 Sequence	
6	34	100.0	34	6	AX710004	AX710004 Sequence	
7	34	100.0	34	6	BD083073	BD083073 Antisense	
8	34	100.0	34	6	BD093612	BD093612 Antisense	
9	34	100.0	44	6	AX710017	AX710017 Sequence	
c 10	34	100.0	67	6	AX710015	AX710015 Sequence	
11	34	100.0	78	6	AX114851	AX114851 Sequence	
c 12	34	100.0	79	6	AX114852	AX114852 Sequence	
13	34	100.0	94	6	AX652254	AX652254 Sequence	
14	34	100.0	94	6	AX662260	AX662260 Sequence	
15	34	100.0	7175	6	AX114853	AX114853 Sequence	
16	34	100.0	8153	6	AX114871	AX114871 Sequence	
17	34	100.0	8811	12	AY569779	AY569779 Cloning	
18	34	100.0	9479	12	AY569778	AY569778 Cloning	
19	34	100.0	12404	12	AY569780	AY569780 Cloning	

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RESULT 2
BD185623
LOCUS      BD185623          34 bp      DNA      linear      PAT 17-JUN-2003
DEFINITION Knockout animal.
ACCESSION  BD185623
VERSION    BD185623.1 GI:31877823
KEYWORDS   JP 2002369689-A/2.
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 34)
AUTHORS   Ide,H., Yamamura,K. and Araki,K.
TITLE     Knockout animal
JOURNAL   Patent: JP 2002369689-A 2 24-DEC-2002;
          JAPAN SCIENCE AND TECHNOLOGY CORP,EU GENE LTD, PRESIDENT OF
          KUMAMOTO UNIVERSITY
COMMENT   OS Artificial Sequence
          PN JP 2002369689-A/2
          PD 24-DEC-2002
          PF 25-MAY-2001 JP 2001157568
          PI HIROYUKI IDE,KENICHI YAMAMURA,KIMI ARAKI
          PC C12N15/09,A01K67/027,C12N5/10,C12N15/00,C12N5/00 CC
          Description of Artificial Sequence:synthetic DNA FH Key
          Location/Qualifiers
          FT source
          1..34
          /organism='Artificial Sequence'.
FEATURES   source
          Location/Qualifiers
          1..34
          /organism="synthetic construct"
          /mol_type="genomic DNA"
          /db_xref="taxon:32630"
ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34
    |||||
Db 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34

RESULT 3
AX114842
LOCUS      AX114842          34 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION Sequence 2 from Patent WO0129208.
ACCESSION  AX114842
VERSION    AX114842.1 GI:14031784
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE     Conditional gene trapping construct for the disruption of genes
JOURNAL   Patent: WO 0129208-A 2 26-APR-2001;
          ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES   Location/Qualifiers
          source
          1..34
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="mutant loxp site - lox66"
ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34
    |||||
Db 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34

RESULT 4
AX137068
LOCUS      AX137068          34 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 2 from Patent EP1092768.
ACCESSION  AX137068
VERSION    AX137068.1 GI:14273413
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Kuehn,R. and von Melchner,H.
TITLE     Conditional gene trapping construct for the disruption of genes
JOURNAL   Patent: EP 1092768-A 2 18-APR-2001;
          ARTEMIS Pharmaceuticals GmbH (DE) ; FrankGen Biotechnologie AG (DE)
FEATURES   Location/Qualifiers
          source
          1..34
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="mutant loxp site - lox66"
ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34
    |||||
Db 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34

RESULT 5
AX540641
LOCUS      AX540641          34 bp      DNA      linear      PAT 23-NOV-2002
DEFINITION Sequence 10 from Patent WO0240685.
ACCESSION  AX540641
VERSION    AX540641.1 GI:25273630
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
other sequences; artificial sequences.
REFERENCE  1
AUTHORS   Xin,H.B. and Kotlikoff,M.
TITLE     Vectors for conditional gene inactivation
JOURNAL   Patent: WO 0240685-A 10 23-MAY-2002;
          CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES   Location/Qualifiers
          source
          1..34
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="A mutant loxp sequence"
ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34
    |||||
Db 1 ATAACTTCGTATAGCATACATTATTACGAACGGTA 34

RESULT 6
AX710004
LOCUS      AX710004          34 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 1 from Patent EP1288295.
ACCESSION  AX710004
VERSION    AX710004.1 GI:29786615
KEYWORDS   .
SOURCE     synthetic construct
```


ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Altmann,M., Neuhierl,B. and Hammerschmidt,W.
TITLE Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL Patent: EP 1288295-A 1 05-MAR-2003;
GSP-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)

FEATURES
Location/Qualifiers
1..34
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid lox 66 ohne flanks"

ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
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Db 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 7
BD083073
LOCUS BD083073 34 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense type gene trap vector.
ACCESSION BD083073
VERSION BD083073.1 GI:22628683
KEYWORDS JP 2001321174-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 34)
AUTHORS Taniguchi,K. and Karasawa,M.
TITLE Antisense type gene trap vector
JOURNAL Patent: JP 2001321174-A 3 20-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Artificial Sequence
PN JP 2001321174-A/3
PD 20-NOV-2001
PF 11-MAY-2000 JP 2000138938
PI KATSUMI TANIGUCHI,MIKA KARASAWA
PC C12N15/09,A01K67/027,C12N5/10/(C12N5/10,C12R1:91),C12N15/00,
PC C12N5/00,
PC C12N5/00,C12R1:91)
CC Description of Artificial Sequence:lox66 sequence FH Key
Location/Qualifiers
1..34
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1..34
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 8
BD093612
LOCUS BD093612 34 bp DNA linear PAT 27-AUG-2002
DEFINITION Antisense gene trap vector.
ACCESSION BD093612
VERSION BD093612.1 GI:22639200
KEYWORDS WO 0185973-A/3.

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 34)
AUTHORS Taniguchi,M. and Karasawa,M.
TITLE Antisense gene trap vector
JOURNAL Patent: WO 0185973-A 3 15-NOV-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,MASARU TANIGUCHI,MIKA KARASAWA

COMMENT OS Artificial Sequence
PN WO 0185973-A/3
PD 15-NOV-2001
PF 29-AUG-2000 WO 2000JP005824
PR 11-MAY-2000 JP OOP 138938
PI MASARU TANIGUCHI,MIKA KARASAWA
PC C12N15/85,C12N5/10,A01K67/027//A61K48/00
CC Description of Artificial Sequence:lox66 sequence FH Key
Location/Qualifiers
1..34
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 9
AX710017
LOCUS AX710017 44 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 14 from Patent EP1288295.
ACCESSION AX710017
VERSION AX710017.1 GI:29786628
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Altmann,M., Neuhierl,B. and Hammerschmidt,W.
TITLE Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL Patent: EP 1288295-A 14 05-MAR-2003;
GSP-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)

FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid lox 66 mit flanks"

ORIGIN
Query Match 100.0%; Score 34; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 6 ATAACCTTCGTATAGCATACATTATACGAACGGTA 39

RESULT 10
AX710015/c
LOCUS AX710015 67 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 12 from Patent EP1288295.
ACCESSION AX710015
VERSION AX710015.1 GI:29786626
KEYWORDS

```

SOURCE      synthetic construct
ORGANISM     synthetic construct
other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Altmann,M., Neuhierl,B. and Hammerschmidt,W.
TITLE        Use of mutated recognition sites for multiple successive recombina
se-mediated recombinations in a genetic system
JOURNAL      Patent: EP 1288295-A 12 05-MAR-2003;
GSP-Forschungszentrum fuer Umwelt und Gesundheit GmbH (DE)
FEATURES     source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonukleotid"

ORIGIN

Query Match      100.0%; Score 34; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 43 ATAACTTCGTATAGCATACATTATACGAACGGTA 10

RESULT 11
AX114851
LOCUS          AX114851              78 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION     Sequence 11 from Patent WO0129208.
ACCESSION      AX114851
VERSION        AX114851.1 GI:14031793
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Kuehn,R., von Melchner,H. and Altschmied,J.
TITLE          Conditional gene trapping construct for the disruption of genes
JOURNAL        Patent: WO 0129208-A 11 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES       source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer lox3"

ORIGIN

Query Match      100.0%; Score 34; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 5 ATAACTTCGTATAGCATACATTATACGAACGGTA 38

RESULT 12
AX114852/c
LOCUS          AX114852              79 bp      DNA      linear      PAT 11-MAY-2001
DEFINITION     Sequence 12 from Patent WO0129208.
ACCESSION      AX114852
VERSION        AX114852.1 GI:14031794
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Kuehn,R., von Melchner,H. and Altschmied,J.
TITLE          Conditional gene trapping construct for the disruption of genes
JOURNAL        Patent: WO 0129208-A 12 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)

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FEATURES     source
            Location/Qualifiers
            1. .79
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            /db_xref="taxon:32630"
            /note="primer lox4"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 79 ATAACTTCGTATAGCATACATTATACGAACGGTA 46

RESULT 13
AX662254
LOCUS          AX662254              94 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION     Sequence 10 from Patent WO02083889.
ACCESSION      AX662254
VERSION        AX662254.1 GI:29163153
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE          Methods
JOURNAL        Patent: WO 02083889-A 10 24-OCT-2002;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES       source
            1. .94
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

ORIGIN

Query Match      100.0%; Score 34; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43

RESULT 14
AX662260
LOCUS          AX662260              94 bp      DNA      linear      PAT 22-MAR-2003
DEFINITION     Sequence 16 from Patent WO02083889.
ACCESSION      AX662260
VERSION        AX662260.1 GI:29163159
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Bigger,B.W., Tolmachov,O. and Coutelle,C.
TITLE          Methods
JOURNAL        Patent: WO 02083889-A 16 24-OCT-2002;
IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES       source
            1. .94
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

ORIGIN

Query Match      100.0%; Score 34; DB 6; Length 94;

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Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 10 ATAACTTCGTATAGCATACATTATACGAACGGTA 43

RESULT 15
AX114853
LOCUS AX114853 7175 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 13 from Patent WO0129208.
ACCESSION AX114853
VERSION AX114853.1 GI:14031795
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
1 other sequences; artificial sequences.
REFERENCE
AUTHORS Kuehn,R., von Melchener,H. and Altschmied,J.
TITLE Conditional gene trapping construct for the disruption of genes
JOURNAL Patent: WO 0129208-A 13 26-APR-2001;
ARTEMIS Pharmaceuticals GmbH (DE) ; Frankgen Biotechnologie AG (DE)
FEATURES
source
1. 7175
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="vector pRK57SA-beta"

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 7175;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
|||||
Db 446 ATAACTTCGTATAGCATACATTATACGAACGGTA 479

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OM nucleic - nucleic search, using sw model

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5: Geneseqn2001bs:*
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7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	5	AAD04916
2	34	100.0	34	6	ABN84176
3	34	100.0	34	6	ABA03776
4	34	100.0	34	8	ABV75996
5	34	100.0	34	8	ABZ20924
6	34	100.0	34	8	ABZ79445
7	34	100.0	34	9	ACC85308
8	34	100.0	34	10	ADD13801
9	34	100.0	34	10	ADD15150
10	34	100.0	34	10	ABZ75320
11	34	100.0	44	8	ABZ20935
12	34	100.0	67	8	ABZ20923
13	34	100.0	78	5	AAD04925
14	34	100.0	79	5	AAD04926
15	34	100.0	94	8	ABV75994
16	34	100.0	94	8	ABV75989
17	34	100.0	7175	5	AAD04927
18	34	100.0	8153	5	AAD04945
19	32.4	95.3	34	8	ABZ20925
20	30.8	90.6	34	8	ABZ20926

21	30.8	90.6	34	9	ACC85310
22	30.4	89.4	37	6	AAD31540
23	30	88.2	40	4	AHH44859
24	29.2	85.9	34	8	ABZ20927
25	29.2	85.9	68	5	AHH20921
26	29.2	85.9	722	9	ADA12883
27	29	85.3	29	4	AHH41178
28	29	85.3	29	7	ADL18608
29	29	85.3	34	2	AAQ47238
30	29	85.3	34	2	AAQ47239
31	29	85.3	34	2	AAQ94929
32	29	85.3	34	2	AAT42300
33	29	85.3	34	2	AAT42299
34	29	85.3	34	2	AAT36911
35	29	85.3	34	2	AAT92195
36	29	85.3	34	2	AAT90585
37	29	85.3	34	2	AAV17069
38	29	85.3	34	2	AAV76189
39	29	85.3	34	2	AAV61038
40	29	85.3	34	2	AAV76039
41	29	85.3	34	2	AAV19902
42	29	85.3	34	3	AAV58294
43	29	85.3	34	3	AAV58293
44	29	85.3	34	3	AAZ58066
45	29	85.3	34	3	AAZ58071

ALIGNMENTS

RESULT 1

AAD04916

ID AAD04916 standard; DNA; 34 BP.

AC AAD04916;

DT 17-JUL-2001 (first entry)

DE Recombinase recognition sequence (RRS), loxP site mutant (lox66) DNA.

KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; mutant; ds.

OS Enterobacteria phage P1.

OS Synthetic.

XX WO200129208-A1.

XX 26-APR-2001.

XX 16-OCT-2000; 2000WO-EP010162.

XX 16-OCT-1999; 99EP-00120592.

XX 27-OCT-1999; 99US-0162016P.

XX (ARTE-) ARTEMIS PHARM GMBH.

XX (FRAN-) FRANKEN BIOTECHNOLOGIE AG.

XX Kuehn R, Von Melchner H, Altschmied J;

XX WPI; 2001-308486/32.

XX New gene trapping construct capable of causing conditional mutations in genes, comprises functional DNA segment inserted in sense or antisense direction relative to gene to be trapped.

XX Claim 4; Page 49; 78pp; English.

XX The present invention relates to a conditional gene trapping construct capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by two recombinase recognition sequences (RRSs) specific to site specific

CC recombinase which is capable of unidirectional inversion of double
 CC standard DNA segment. One of the DNA segment (disruption cassette) is
 CC inserted in antisense orientation relative to the transcriptional
 CC orientation of the gene to be trapped. The other DNA segment (selection
 CC cassette) is inserted in sense direction relative to the transcriptional
 CC orientation of the gene to be trapped. The cell comprising the gene
 CC trapping construct is useful for the identification and/or isolation of
 CC genes. The transgenic organism comprising the gene trapping construct is
 CC useful to study gene function at various developmental stages. The gene
 CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present DNA sequence encodes recombinase recognition sequence,
 CC loxP site mutant (lox66'), which flanks the functional DNA segments of
 CC gene trapping construct
 XX
 SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 100.0%; Score 34; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 Db 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 RESULT 2
 ID ABN84176 standard; DNA; 34 BP.
 AC ABN84176;
 XX
 DT 23-SEP-2002 (first entry)
 DE LoxP right element mutant.
 XX
 KW Gene inactivation; mutagenesis; vector; knockout animal;
 KW transgenic animal; gene trapping; loxP; mutant; ss.
 XX
 OS Enterobacteria phage P1.
 OS Synthetic.
 XX
 PN WO200240685-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 16-NOV-2001; 2001WO-US043916.
 XX
 PR 16-NOV-2000; 2000US-0249200P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Xin H, Kotlikoff M;
 XX
 DR WPI; 2002-537342/57.
 XX
 PT Novel genetically engineered vector comprising gene trap cassette, and
 PT mutational element cassette that is transcriptionally silent, but which
 PT is activated by recombinase expression to disrupt expression of trapped
 PT gene.
 XX
 PS Example 2; Page 35; 58pp; English.
 XX
 CC The present invention provides recombinant vectors and methods of using
 CC the vectors in a high-throughput genetic system to rapidly generate
 CC conditional and/or conventional knockout mutants, e.g. in mice, useful
 CC for identifying and defining mammalian gene function in vivo. The methods
 CC combine gene trapping, gene targeting, and site-specific recombinational
 CC techniques. The vectors comprise a transcriptionally silent mutational
 CC element that is inserted within a gene in a target cell in a manner that
 CC retains gene function, and which can be manipulated to inactivate the
 CC gene when desired. The mutational element may be flanked by mutant loxP
 CC sites in a manner that produces a directional bias toward inversion of
 CC the mutational sequence upon exposure to cre recombinase. Once inverted,

CC the mutational element is spliced into the trapped gene resulting in
 CC expression of a reporter gene and premature termination of the endogenous
 CC mRNA. Site-directed DNA integration is achieved using a pair of mutant
 CC loxP sites, a right element (RE) mutant (present sequence) and a left
 CC element (LE) mutant (see ABN84175). The mutant loxP system produces a
 CC reaction biased toward an irreversible gene inversion. The method of the
 CC invention facilitates investigation of the function of individual genes
 CC by a rapid extension of the conditional knockout approach
 XX
 SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 100.0%; Score 34; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 Db 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 RESULT 3
 ID ABA03776 standard; DNA; 34 BP.
 AC ABA03776;
 XX
 DT 19-FEB-2002 (first entry)
 DE Synthetic lox66 sequence.
 XX
 KW lox66; gene therapy; gene targeting; gene trapping;
 KW antisense RNA production; ds.
 XX
 OS Synthetic.
 XX
 PN WO200185973-A1.
 XX
 PD 15-NOV-2001.
 XX
 PF 29-AUG-2000; 2000WO-JP005824.
 XX
 PR 11-MAY-2000; 2000JP-00138938.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Taniguchi M, Karasawa M;
 XX
 DR WPI; 2002-055602/07.
 XX
 PT Antisense type gene trap vector, useful for gene therapy of diseases and
 PT production of animal models for disease study, disrupts transcription of
 PT specific gene.
 XX
 PS Claim 19; Page 43; 48pp; Japanese.
 XX
 CC The invention relates to a method for producing cells in which the
 CC expression of a gene is disrupted. The cells are transformed with a gene
 CC trap vector to give a trap clone having the vector inserted at a specific
 CC mutation site of the target gene. The trap clone is then transformed with
 CC a vector that inserts a promoter in the antisense direction of the gene,
 CC enforcing transcription of antisense RNA. The method is useful for the
 CC production of animal models for studying human diseases. It is also
 CC useful as gene therapy for the treatment and prevention of diseases. The
 CC present sequence is a lox66 sequence claimed in the specification
 XX
 SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
 Query Match 100.0%; Score 34; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34

Db 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34

RESULT 4
ABV75996
ID ABV75996 standard; DNA; 34 BP.

XX AC ABV75996;
XX DT 11-FEB-2003 (first entry)
XX DE Modified right element loxp site.
XX KW LoxP; phage P1; recombination; minicircle; gene therapy; mitochondria;
XX KW mutant; ss.
XX OS Bacteriophage p1.
XX OS Synthetic.
XX PN WO200283889-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-GB001668.
XX PR 10-APR-2001; 2001GB-00008968.
XX PR 05-OCT-2001; 2001US-0327029P.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Bigger BW, Tolmachov O, Coutelle C;
XX WPI; 2003-075546/07.
XX DT New cell capable of expressing an endonuclease, useful for producing a
PT minicircle for mitochondrial gene therapy, comprises a parent plasmid
PT capable of recombination to form a minicircle and a miniplasmid.
XX PS Disclosure; Fig 4; 70pp; English.
XX CC The present sequence is that of a right element (RE) loxp site in which
CC the 5 nucleotides at the 3' end of loxp have been modified. The RE loxp
CC site is used in the method of the invention for the production of a
CC minicircle. In this method, a parent plasmid is provided which has a
CC nucleic acid sequence flanked by recombination sites. The plasmid is
CC exposed to an enzyme which causes recombination at the recombination
CC sites, forming (i) a minicircle comprising the nucleic acid sequence and
CC (ii) a miniplasmid comprising the remainder of the parent plasmid. One
CC recombination site is modified at the 5' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, and the other
CC recombination site is modified at the 3' end such that its reaction with
CC the enzyme is less efficient than the wild-type site, both modified sites
CC being located in the minicircle after recombination. This favours the
CC formation of the minicircle. In a preferred embodiment, the enzyme is Cre
CC recombinase and the recombination sites are loxp sites. The method is
CC preferably carried out in a bacterium, especially Escherichia coli. The
CC minicircle can be used for mitochondrial gene therapy

XX SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 100.0%; Score 34; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34
DB 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34

RESULT 6
ABZ79445
ID ABZ79445 standard; DNA; 34 BP.
XX AC ABZ79445;
XX DT 23-MAY-2003 (first entry)
XX DE Lox 66 DNA # SEQ ID 2.
XX KW LoxP; lox 66; knockout mouse; vascularisation; embryonic stem cell;
XX KW drug development; locus of crossing over; ds.
XX OS Synthetic.
XX PN JP2002369689-A.
XX PD 24-DEC-2002.
XX PF 25-MAY-2001; 2001JP-00157568.
XX PF 25-MAY-2001; 2001JP-00157568.

AC ABZ20924;
XX DT 10-APR-2003 (first entry)
XX DE LoxP mutant with flanking sequence oligonucleotide #1.
XX KW Non-identical recognition sequence mutant; sequence-specific recombinase;
XX KW recombination; antibiotic-resistance marker; loxp; PCR; primer; ss.
XX OS Unidentified.
XX PN DE10140030-C1.
XX PD 19-DEC-2002.
XX PF 16-AUG-2001; 2001DE-01040030.
XX PR 16-AUG-2001; 2001DE-01040030.
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
XX PI Altmann M, Neuhierl B, Hammerschmidt W;
XX WPI; 2003-048025/05.
XX DT Method for performing multiple recombination events in a genetic system,
PT useful e.g. for removing antibiotic resistance genes, uses mutant
PT recombinase recognition sites.
XX PS Claim 3; Col 9; 10pp; German.
XX CC The present invention relates to the use of two non-identical recognition
CC sequence mutants for a sequence-specific recombinase for performing two
CC or more recombination events, mediated by the sequence-specific
CC recombinase, in a single genetic system. The method is used to manipulate
CC genetic systems (microbial, plant or animal) by site-specific
CC recombination, e.g. to insert or remove DNA and most particularly to
CC remove antibiotic-resistance markers. The present sequence was used to
CC isolate the loxp coding sequence in the exemplification of the invention

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (IDSH/) IDE H.
PA (YAMA/) YAMAMURA K.
PA (ARAK/) ARAKI Y.
XX
DR WPI; 2003-125824/12.
XX
XX Knockout mouse or embryonic stem cells with introduced trap vectors
PT containing a loxp sequence or a variant loxp sequence with disrupted gene
PT of sequence No. 7 of 1405 bases.
XX
XX Claim 5; Fig 4; 21pp; Japanese.
XX
XX The invention relates to a knockout mouse or embryonic stem cells with
CC introduced trap vectors containing a loxp sequence. The knockout animals
CC of the invention may be used in the analysis of genomic functions,
CC particularly for investigating the processes of vascularisation and the
CC development of drugs participating in such processes. The current
CC sequence represents lox 66
XX
XX Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 34; DB 8; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATAACCTTCGTATAGCATACATTATACGAAACGGTA 34
Db 1 ATAACCTTCGTATAGCATACATTATACGAAACGGTA 34
RESULT 7
ACC85308
ID ACC85308 standard; DNA; 34 BP.
XX
AC ACC85308;
XX
DT 18-SEP-2003 (first entry)
XX
DE Recombinase lox66 DNA recognition sequence.
XX
XX Vegetable plasmid transformation; transgenic; recognition sequence;
KW plant; site-specific integration; nutrition; seed production;
KW chemical production; ds.
XX
OS Unidentified.
XX
XX WO2003054201-A1.
XX
XX 03-JUL-2003.
XX
XX 16-DEC-2002; 2002WO-BF014303.
XX
XX 20-DEC-2001; 2001DE-01063159.
XX
XX (SUNG-) SUNGENE GMBH & CO KGAA.
XX
XX Biesgen C;
PI
XX WPI; 2003-541820/51.
XX
XX Site-specific integration of DNA into plasmid DNA, useful for making
PT transgenic plants used e.g. as food, by recombinase-mediated insertion.
PT
XX Disclosure; Page 35; 164pp; German.
XX
XX The present invention relates to a method for the site-specific
CC integration of a DNA sequence into the plasmid DNA of a plant or its
CC derived cells. Transgenic plants in which a DNA sequence has been
CC integrated, also their cell cultures, organs, tissues etc. are useful in
CC human or animal nutrition, to produce seeds, and to produce
CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,

CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
CC present sequence is a recognition sequence shown in the exemplification
CC of the invention
XX
SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 100.0%; Score 34; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATAACCTTCGTATAGCATACATTATACGAAACGGTA 34
Db 1 ATAACCTTCGTATAGCATACATTATACGAAACGGTA 34
RESULT 8
ADD13801/c
ID ADD13801 standard; DNA; 34 BP.
XX
AC ADD13801;
XX
DT 01-JAN-2004 (first entry)
XX
XX Oligonucleotide lox66 DNA.
XX
XX library; transfection; humanized monoclonal antibody; antigen;
KW T cell receptor; primer; ss.
XX
OS Synthetic.
XX
XX EP1298207-A1.
XX
XX 02-APR-2003.
XX
XX 01-OCT-2001; 2001EP-00123596.
XX
XX 01-OCT-2001; 2001EP-00123596.
XX
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
XX Breitling F, Moldenhauer G, Poustka A, Kuehlwein T;
XX WPI; 2003-383833/37.
XX
XX Preparing library of protein-producing eukaryotic cells, useful for
PT producing humanized high-affinity antibodies, comprises introducing
PT specific recombination signals into chromosomal gene loci and integrating
PT a variety of DNA sequences.
XX
XX Example 7; Page 15; 75pp; German.
XX
XX This invention describes a novel method of preparing a library of protein
CC -producing eukaryotic cells comprising (a) introducing specific
CC recombination signals into one or two chromosomal gene loci, (b)
CC Expanding at least one of the modified cells, (c) Transfecting many
CC different DNA sequences, each flanked by recombination signals, into the
CC expanded cells and (d) integrating the DNA sequences into the gene loci
CC on the basis of the recombination signals and the appropriate
CC recombinase. The resulting cells express different proteins, each from an
CC integrated DNA sequence and the proteins are bound to the cell surface.
CC The method is particularly used to produce libraries of humanized
CC monoclonal antibodies, for selection of those with affinity for
CC particular antigens and useful for diagnostic or therapeutic use.
CC Libraries of T cell receptors may also be prepared. The method produces
CC libraries of high diversity; provides easy, quick and automatable
CC selection from a large number of proteins, allows relatively simple
CC alteration of the expressed gene (e.g. fusion to other protein-coding
CC sequences), is suitable for large scale protein production and allows
CC simple verification and characterization of selected cell lines. The
CC method does not require incorporation of a resistance marker. This
CC sequence represents oligonucleotide lox66.
XX
XX Sequence 34 BP; 10 A; 5 C; 6 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
 |||||
 DB 34 ATAACTTCGTATAGCATACATTATACGAACGGTA 1

RESULT 9
 ADD15150
 ID ADD15150 standard; DNA; 34 BP.
 AC
 XX
 AC ADD15150;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Variant loxP DNA recombination site designated lox66 (SeqID 2).
 XX
 KW loxP site; circular; transgenic; plant; non-replicating; transgene;
 KW growth regulant; insect resistance; fungal disease resistance;
 KW stress resistance; ss; lox66.
 XX
 OS Unidentified.
 XX
 PN US2003100077-A1.
 XX
 PD 29-MAY-2003.
 XX
 PF 20-SEP-2001; 2001US-00957660.
 XX
 PR 20-SEP-2001; 2001US-00957660.
 XX
 PA (KORT/) KORTE J A.
 PA (LOWE/) LOWE B A.
 XX
 PI Korte JA, Lowe BA;
 XX
 DR WPI; 2003-777313/73.
 XX
 PT Preparing a non-replicating, circular nucleic acid molecule useful for
 transforming crop plants to add desirable trait such as herbicide
 resistance, by amplifying starting circular nucleic acid molecule.
 XX
 PS Claim 11; SEQ ID NO 2; 66pp; English.
 XX
 CC This invention relates to an in vitro method to create circular molecules
 for use in transformation for the generation of transgenic plants.
 CC Specifically, it refers to a preparing a non-replicating, circular
 CC nucleic acid molecule using a first non-mutagenizing oligonucleotide
 CC primer with a nucleic acid sequence complementary to a selected sequence
 CC of the starting circular DNA molecule. As such, the present invention
 CC describes a method useful for preparing a fertile transgenic plant
 CC derived from a dicotyledonous plant preferably soybean and the transgenic
 CC cell is from a monocotyledon, preferably maize. The transgene can be a
 CC plant growth regulant with a selectable phenotype that confers an
 CC advantageous trait, for example, insect resistance, bacterial or fungal
 CC disease resistance, enhanced nutrient utilisation or stress resistance.
 CC This oligonucleotide sequence is a variant of the wild type loxP DNA
 CC recombination site known as lox66, used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
 |||||
 DB 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 11
 ABZ20935
 ID ABZ20935 standard; DNA; 44 BP.
 AC
 XX
 AC ABZ20935;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Lox66 isolation oligonucleotide.
 XX
 KW Non-identical recognition sequence mutant; sequence-specific recombinase;
 KW recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
 XX
 OS Unidentified.
 XX
 PN DE10140030-C1.
 XX
 PD 19-DEC-2002.
 XX

RESULT 10
 ABZ75320
 ID ABZ75320 standard; DNA; 34 BP.
 XX
 AC ABZ75320;
 XX
 DT 29-APR-2003 (first entry)
 XX
 DE Lox66 related sequence.
 XX
 KW Lox66; knockout animal; Tubedown-1; genomic function analysis;
 KW organ development; ds.
 XX
 OS Unidentified.
 XX
 PN JP2002345477-A.
 XX
 PD 03-DEC-2002.
 XX
 PF 25-MAY-2001; 2001JP-00157567.
 XX
 PR 25-MAY-2001; 2001JP-00157567.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (IDEH/) IDE H.
 PA (YAMA/) YAMAMURA K.
 PA (ARAK/) ARAKI Y.
 XX
 DR WPI; 2003-072475/07.
 XX
 PT Knockout animals with introduced a trap vector containing a variant loxP
 with introduced variation in a part of sequence(s) of a spacer sequence,
 and reverse repetitive sequence 1 and/or 2.
 XX
 PS Claim 4; Page 12; 22pp; Japanese.
 XX
 CC The invention relates to novel knockout animals with the disrupted
 CC Tubedown-1 gene. The transgenic animals of the invention are useful for
 CC analysis of genomic functions, and establishment of an analytic system
 CC for the development of organs. The present sequence is related to Lox66
 XX
 SQ Sequence 34 BP; 13 A; 6 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 34; DB 10; Length 34;
 Best Local Similarity 100.0%; Pred. No. 0.00023;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
 |||||
 DB 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 11
 ABZ20935
 ID ABZ20935 standard; DNA; 44 BP.
 AC
 XX
 AC ABZ20935;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE Lox66 isolation oligonucleotide.
 XX
 KW Non-identical recognition sequence mutant; sequence-specific recombinase;
 KW recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
 XX
 OS Unidentified.
 XX
 PN DE10140030-C1.
 XX
 PD 19-DEC-2002.
 XX

```

PF 16-AUG-2001; 2001DE-01040030.
XX
PR 16-AUG-2001; 2001DE-01040030.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
PI Altmann M, Neuhierl B, Hammerschmidt W;
XX WPI; 2003-048025/05.
XX
PT Method for performing multiple recombination events in a genetic system,
PT useful e.g. for removing antibiotic resistance genes, uses mutant
PT recombinase recognition sites.
XX
PS Example; Fig 1; 10pp; German.
XX
CC The present invention relates to the use of two non-identical recognition
CC sequence mutants for a sequence-specific recombinase for performing two
CC or more recombination events, mediated by the sequence-specific
CC recombinase, in a single genetic system. The method is used to manipulate
CC genetic systems (microbial, plant or animal) by site-specific
CC recombination, e.g. to insert or remove DNA and most particularly to
CC remove antibiotic-resistance markers. The present sequence was used to
CC isolate the lox66 and lox71 coding sequences in the exemplification of
CC the invention
XX
SQ Sequence 44 BP; 14 A; 10 C; 6 G; 14 T; 0 U; 0 Other;
Query Match 100.0%; Score 34; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATAACCTCGTATAGCATACATTATACGACGGTA 34
DB 6 ATAACCTCGTATAGCATACATTATACGACGGTA 39
RESULT 12
ABZ20923/C
ID ABZ20923 standard; DNA; 67 BP.
XX
AC ABZ20923;
XX
DT 10-APR-2003 (first entry)
XX
DE Lox66 and lox71 isolation oligonucleotide #2.
XX
KW Non-identical recognition sequence mutant; sequence-specific recombinase;
KW recombination; antibiotic-resistance marker; lox66; lox71; PCR; primer;
KW ss.
XX
OS Unidentified.
XX
PN DE10140030-C1.
XX
PD 19-DEC-2002.
XX
PF 16-AUG-2001; 2001DE-01040030.
XX
PR 16-AUG-2001; 2001DE-01040030.
XX
PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.
PI Altmann M, Neuhierl B, Hammerschmidt W;
XX WPI; 2003-048025/05.
XX
PT Method for performing multiple recombination events in a genetic system,
PT useful e.g. for removing antibiotic resistance genes, uses mutant
PT recombinase recognition sites.
XX
PS Example; Col 6; 10pp; German.
XX

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CC The present invention relates to the use of two non-identical recognition
CC sequence mutants for a sequence-specific recombinase for performing two
CC or more recombination events, mediated by the sequence-specific
CC recombinase, in a single genetic system. The method is used to manipulate
CC genetic systems (microbial, plant or animal) by site-specific
CC recombination, e.g. to insert or remove DNA and most particularly to
CC remove antibiotic-resistance markers. The present sequence was used to
CC isolate the lox66 and lox71 coding sequences in the exemplification of
CC the invention
XX
SQ Sequence 67 BP; 20 A; 15 C; 16 G; 16 T; 0 U; 0 Other;
Query Match 100.0%; Score 34; DB 8; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATAACCTCGTATAGCATACATTATACGACGGTA 34
DB 43 ATAACCTCGTATAGCATACATTATACGACGGTA 10
RESULT 13
AAD04925
ID AAD04925 standard; DNA; 78 BP.
XX
AC AAD04925;
XX
DT 17-JUL-2001 (first entry)
XX
DE Primer lox3 for synthesising DNA fragment with loxP mutant sites.
XX
KW Gene trapping construct; conditional mutation; unidirectional inversion;
KW recombinase recognition sequence; RRS; disruption cassette;
KW selection cassette; transgenic organism; loxP site; primer; ss.
XX
OS Enterobacteria phage P1.
OS Synthetic.
XX
PN WO200129208-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-EP010162.
XX
PR 16-OCT-1999; 99EP-00120592.
PR 27-OCT-1999; 99US-0162016P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
XX
PI Kuehn R, Von Melchner H, Altschmied J;
XX WPI; 2001-308486/32.
XX
PT New gene trapping construct capable of causing conditional mutations in
PT genes, comprises functional DNA segment inserted in sense or antisense
PT direction relative to gene to be trapped.
XX
PS Example 1; Page 18; 78pp; English.
XX
CC The present invention relates to a conditional gene trapping construct
CC capable of causing conditional mutations in genes. The gene trapping
CC construct comprises two functional DNA segments, each being flanked by
CC two recombinase recognition sequences (RRSs) specific to site specific
CC recombinase which is capable of unidirectional inversion of double
CC standard DNA segment. One of the DNA segment (disruption cassette) is
CC inserted in antisense orientation relative to the transcriptional
CC orientation of the gene to be trapped. The other DNA segment (selection
CC cassette) is inserted in sense direction relative to the transcriptional
CC orientation of the gene to be trapped. The cell comprising the gene
CC trapping construct is useful for the identification and/or isolation of
CC genes. The transgenic organism comprising the gene trapping construct is
CC useful to study gene function at various developmental stages. The gene

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CC trapping construct is useful for mutationally inactivating all cellular
 CC genes. The present sequence is a primer lox3 which is used for
 CC synthesising a DNA fragment containing a lox66 and a lox71 Cre
 CC recombinase recognition mutant sites in opposite orientation. The primer
 CC is used for constructing the gene trap vector pRK57SA-beta
 XX Sequence 78 BP; 27 A; 14 C; 14 G; 23 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 34; DB 5; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 DB 5 ATAACCTTCGTATAGCATACATTATACGAACGGTA 38

RESULT 14
 AAD04926/c
 ID AAD04926 standard; DNA; 79 BP.
 XX AC AAD04926;
 XX DT 17-JUL-2001 (first entry)
 XX DE Primer lox4 for synthesising DNA fragment with loxP mutant sites.
 XX KW Gene trapping construct; conditional mutation; unidirectional inversion;
 XX KW recombinase recognition sequence; RRS; disruption cassette;
 XX KW selection cassette; transgenic organism; loxP site; primer; ss.
 XX OS Enterobacteria phage P1.
 XX OS Synthetic.
 XX PN WO200129208-A1.
 XX PD 26-APR-2001.
 XX PF 16-OCT-2000; 2000WO-EP010162.
 XX PR 16-OCT-1999; 99EP-00120592.
 XX PR 27-OCT-1999; 99US-0162016P.
 XX PA (ARTE-) ARTEMIS PHARM GMBH.
 XX PA (FRAN-) FRANKGEN BIOTECHNOLOGIE AG.
 XX PI Kuehn R, Von Melchener H, Altschmied J;
 XX WPI; 2001-308486/32.
 XX New gene trapping construct capable of causing conditional mutations in
 XX genes, comprises functional DNA segment inserted in sense or antisense
 XX direction relative to gene to be trapped.
 XX Example 1; Page 18-19; 78pp; English.
 XX The present invention relates to a conditional gene trapping construct
 XX capable of causing conditional mutations in genes. The gene trapping
 XX construct comprises two functional DNA segments, each being flanked by
 XX two recombinase recognition sequences (RRS) specific to site specific
 XX recombinase which is capable of unidirectional inversion of double
 XX standard DNA segment. One of the DNA segment (disruption cassette) is
 XX inserted in antisense orientation relative to the transcriptional
 XX orientation of the gene to be trapped. The other DNA segment (selection
 XX cassette) is inserted in sense direction relative to the transcriptional
 XX orientation of the gene to be trapped. The cell comprising the gene
 XX trapping construct is useful for the identification and/or isolation of
 XX genes. The transgenic organism comprising the gene trapping construct is
 XX useful to study gene function at various developmental stages. The gene
 XX trapping construct is useful for mutationally inactivating all cellular
 XX genes. The present sequence is a primer lox4 which is used for
 XX synthesising a DNA fragment containing a lox66 and a lox71 Cre
 XX recombinase recognition mutant sites in opposite orientation. The primer

CC is used for constructing the gene trap vector pRK57SA-beta
 XX Sequence 79 BP; 24 A; 14 C; 14 G; 27 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 34; DB 5; Length 79;
 Best Local Similarity 100.0%; Pred. No. 0.00024;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 DB 79 ATAACCTTCGTATAGCATACATTATACGAACGGTA 46

RESULT 15
 ABV75994
 ID ABV75994 standard; DNA; 94 BP.
 XX AC ABV75994;
 XX DT 11-FEB-2003 (first entry)
 XX DE OLIGO-F, contains attP and attB sites for phage phi-C31 integrase.
 XX KW AttP; attB; phage phi-C31; integrase; recombination; minicircle;
 XX KW gene therapy; mitochondria; ss.
 XX OS Bacteriophage phi-C31.
 XX OS Synthetic.
 XX PN WO200283889-A2.
 XX PD 24-OCT-2002.
 XX PF 10-APR-2002; 2002WO-GB001668.
 XX PR 10-APR-2001; 2001GB-00008968.
 XX PR 05-OCT-2001; 2001US-0327029P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Bigger BW, Tolmachov O, Coutelle C;
 XX WPI; 2003-075546/07.
 XX New cell capable of expressing an endonuclease, useful for producing a
 XX minicircle for mitochondrial gene therapy, comprises a parent plasmid
 XX capable of recombination to form a minicircle and a miniplasmid.
 XX Example 3; Page 46; 70pp; English.
 XX The present sequence is that of oligonucleotide OLIGO-F, which was
 XX annealed to OLIGO-R (see ABV75995) and introduced into plasmid pBC-SK(+),
 XX thereby creating attP and attB recombination sites. Minicircle-producing
 XX plasmids with attP and attB sites for phage phi-C31 integrase were
 XX constructed. This is an example of a method of the invention for the
 XX production of a minicircle. In this method, a plasmid having a DNA
 XX sequence flanked by attP and attB sites is exposed to phi-C31 integrase,
 XX thereby forming a minicircle comprising the DNA sequence and a
 XX miniplasmid comprising the remainder of the plasmid. The minicircle is
 XX useful for mitochondrial gene therapy
 XX Sequence 94 BP; 33 A; 19 C; 15 G; 27 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 34; DB 8; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
 DB 10 ATAACCTTCGTATAGCATACATTATACGAACGGTA 43

Search completed: September 8, 2005, 23:11:31

Job time : 201.5 secs

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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 19:07:03 ; Search time 69 Seconds
(without alignments)
806.281 Million cell updates/sec

Title: US-10-030-658B-16
Perfect score: 34
Sequence: 1 ataacttcgtatagcatatattacgaacggtg 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2.6/prodata/1/ina/5B-COMB.seq:*
3: /cgn2.6/prodata/1/ina/6A-COMB.seq:*
4: /cgn2.6/prodata/1/ina/6B-COMB.seq:*
5: /cgn2.6/prodata/1/ina/PCUS-COMB.seq:*
6: /cgn2.6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	29	85.3	29	4	US-09-662-128A-5
2	29	85.3	34	1	US-08-214-023-1
3	29	85.3	34	1	US-08-214-023-2
4	29	85.3	34	1	US-08-615-048-1
5	29	85.3	34	2	US-08-864-224-12
6	29	85.3	34	2	US-08-864-224-17
7	29	85.3	34	2	US-08-743-796-1
8	29	85.3	34	2	US-08-350-260A-1
9	29	85.3	34	2	US-08-350-260A-601
10	29	85.3	34	3	US-08-654-623-4
11	29	85.3	34	3	US-09-011-257-1
12	29	85.3	34	3	US-08-412-777-1
13	29	85.3	34	3	US-08-412-777-2
14	29	85.3	34	3	US-08-412-828-1
15	29	85.3	34	3	US-08-412-828-2
16	29	85.3	34	3	US-09-214-471-1
17	29	85.3	34	3	US-09-193-475-1
18	29	85.3	34	3	US-09-563-239-1
19	29	85.3	34	3	US-09-271-055A-1
20	29	85.3	34	3	US-09-271-055A-2
21	29	85.3	34	3	US-09-603-663-1
22	29	85.3	34	3	US-09-603-663-3
23	29	85.3	34	3	US-09-603-663-5
24	29	85.3	34	3	US-09-603-658-1
25	29	85.3	34	3	US-09-603-658-3
26	29	85.3	34	3	US-09-603-658-5
27	29	85.3	34	3	US-09-602-373A-1

C	28	29	85.3	34	3	US-09-602-373A-3	Sequence 3, Appli
	29	29	85.3	34	3	US-09-602-373A-5	Sequence 5, Appli
	30	29	85.3	34	3	US-09-661-364-1	Sequence 1, Appli
C	31	29	85.3	34	3	US-09-610-259-1	Sequence 1, Appli
C	32	29	85.3	34	3	US-09-610-259-2	Sequence 2, Appli
C	33	29	85.3	34	3	US-09-554-271A-1	Sequence 1, Appli
C	34	29	85.3	34	3	US-09-837-863-1	Sequence 1, Appli
C	35	29	85.3	34	4	US-09-104-337A-1	Sequence 1, Appli
C	36	29	85.3	34	4	US-09-293-303-1	Sequence 1, Appli
C	37	29	85.3	34	4	US-09-718-034-2	Sequence 2, Appli
C	38	29	85.3	34	4	US-09-606-323C-1	Sequence 1, Appli
C	39	29	85.3	34	4	US-09-606-323C-3	Sequence 3, Appli
C	40	29	85.3	34	4	US-09-703-399A-1	Sequence 1, Appli
C	41	29	85.3	34	4	US-09-703-399A-3	Sequence 3, Appli
	42	29	85.3	34	4	US-09-703-399A-5	Sequence 5, Appli
	43	29	85.3	34	4	US-09-377-885A-1	Sequence 1, Appli
C	44	29	85.3	34	4	US-09-377-885A-20	Sequence 20, Appli
	45	29	85.3	34	4	US-09-975-304-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-662-128A-5
; Sequence 5, Application US/09662128A
; Patent No. 6734295
; GENERAL INFORMATION:
; APPLICANT: MIYAGAWA, SHUJI
; APPLICANT: OKABE, MASARU
; TITLE OF INVENTION: MODIFIED CRE RECOMBINASE GENE FOR MAMMALS
; FILE REFERENCE: 197330USO
; CURRENT APPLICATION NUMBER: US/09/662,128A
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: JP11-264364
; PRIOR FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
US-09-662-128A-5

Query Match 85.3%; Score 29; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATATATTACGAA 29
DB 1 ATAACCTCGTATAGCATATATTACGAA 29

RESULT 2
US-08-214-023-1/c
; Sequence 1, Application US/08214023
; Patent No. 5434066
; GENERAL INFORMATION:
; APPLICANT: BEBEE, ROBERT L
; APPLICANT: HARTLEY, JAMES L
; TITLE OF INVENTION: MODULATION OF ENZYME ACTIVITIES IN THE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEIL, GOTSHAL & MANGES
; STREET: 1615 L STREET, N.W.; SUITE 700
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,023
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 59452.0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 682-7033
; TELEFAX: (202) 859-0939
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: ESCHERICHIA COLI
; STRAIN: DH10B
; US-08-214-023-1

Query Match      85.3%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAA 29
DB 34 ATAACTTCGTATAGCATACATTATACGAA 6

RESULT 3
US-08-214-023-2
; Sequence 2, Application US/08214023
; Patent No. 5434066
; GENERAL INFORMATION:
; APPLICANT: BEBEE, ROBERT L
; APPLICANT: HARTLEY, JAMES L
; TITLE OF INVENTION: MODULATION OF ENZYME ACTIVITIES IN THE
; TITLE OF INVENTION: IN VIVO CLONING OF DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEIL, GOTSHAL & MANGES
; STREET: 1615 L STREET, N.W.; SUITE 700
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,023
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
;
;
; NAME: AUERBACH, JEFFREY I
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 59452.0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 682-7033
; TELEFAX: (202) 859-0939
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: ESCHERICHIA COLI
; STRAIN: DH10B
; US-08-214-023-2

Query Match      85.3%; Score 29; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAA 29
DB 1 ATAACTTCGTATAGCATACATTATACGAA 29

RESULT 4
US-08-615-048-1
; Sequence 1, Application US/08615048
; Patent No. 5700470
; GENERAL INFORMATION:
; APPLICANT: Saito, Izumu
; APPLICANT: Kanegae, Yumi
; APPLICANT: Nakai, Michio
; TITLE OF INVENTION: RECOMBINANT DNA VIRUS AND METHOD FOR
; TITLE OF INVENTION: PREPARATION THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,048
; FILING DATE: 12-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-41057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-615-048-1

Query Match      85.3%; Score 29; DB 1; Length 34;
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Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACCTCGTATAGCATACATTATACGAA 29
    |||||
Db 1 ATAACCTCGTATAGCATACATTATACGAA 29

RESULT 5
US-08-864-224-12
; Sequence 12, Application US/08864224
; Patent No. 5851808
; GENERAL INFORMATION:
; APPLICANT: Ellledge, Stephen J.
; APPLICANT: Liu, Qinghua
; TITLE OF INVENTION: Rapid Subcloning Using Site-Specific
; RECOMBINATION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/864,224
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: BCM-02681
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-864-224-17

Query Match 85.3%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAACCTCGTATAGCATACATTATACGAA 29
    |||||
Db 34 ATAACCTCGTATAGCATACATTATACGAA 6

RESULT 7
US-08-743-796-1/c
; Sequence 1, Application US/08743796
; Patent No. 5928914
; GENERAL INFORMATION:
; APPLICANT: Leboulch, P. et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TRANSFORMING CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MTE-198
; TELECOMMUNICATION INFORMATION:

Qy 1 ATAACCTCGTATAGCATACATTATACGAA 29
    |||||
Db 34 ATAACCTCGTATAGCATACATTATACGAA 6

RESULT 6
US-08-864-224-17/c
; Sequence 17, Application US/08864224
; Patent No. 5851808
; GENERAL INFORMATION:
; APPLICANT: Ellledge, Stephen J.
; APPLICANT: Liu, Qinghua
; TITLE OF INVENTION: Rapid Subcloning Using Site-Specific
; RECOMBINATION
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
```

```

; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-743-796-1

Query Match      85.3%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
Db 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 8
US-08-350-260A-1/c
; Sequence 1, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
US-08-350-260A-1

Query Match      85.3%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
Db 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 9
US-08-350-260A-601/c
; Sequence 601, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994

```


; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 601:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-350-260A-601

Query Match 85.3%; Score 29; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
|||||
DB 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 10
US-08-654-623-4/c
; Sequence 4, Application US/08654623
; Patent No. 6010884
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Holliger, Kaspar-Philipp
; APPLICANT: Nissim, Ahuva
; APPLICANT: Fisch, Igor
; APPLICANT: Winter, Gregory P
; TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/654,623
; FILING DATE: 29-MAY-1996
; CLASSIFICATION: 435
; CLASSIFICATION: (C12N 1/21, C12R 1.19)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225453.1
; FILING DATE: 04-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9300816.7
; FILING DATE: 16-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93303614.7
; FILING DATE: 10-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9319969.3
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02492
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9412147.2
; FILING DATE: 17-JUN-1994

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02662
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,418
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33259
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: Other nucleic acid: plasmid DNA
US-08-654-623-4

Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
|||||
DB 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 11
US-09-011-257-1/c
; Sequence 1, Application US/09011257
; Patent No. 6066478
; GENERAL INFORMATION:
; APPLICANT: LUSKY, Monika
; APPLICANT: MEHTALI, Majid
; TITLE OF INVENTION: HELPER VIRUSES FOR PREPARING RECOMBINANT VIRAL VECTORS
; FILE REFERENCE: 017753-090
; CURRENT APPLICATION NUMBER: US/09/011,257
; CURRENT FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: FR 95/09,289
; EARLIER FILING DATE: 1995-07-31
; EARLIER APPLICATION NUMBER: PCT/FR96/01200
; EARLIER FILING DATE: 1996-07-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Bacteriophage P1
US-09-011-257-1

Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
|||||
DB 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 12
US-08-412-777-1/c
; Sequence 1, Application US/08412777
; Patent No. 6091001
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: ZSEBO, KRISZTINA M.
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES USING
; TITLE OF INVENTION: CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:

```
; ADDRESS: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,777
; FILING DATE: 29-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDEL, SARALYNN
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: CELL20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)358-9600 X345
; TELEFAX: (415)349-7392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-412-777-1
;
Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
Db 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 13
US-08-412-777-2/c
; Sequence 2, Application US/08412777
; Patent No. 6091001
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: ZSEBO, KRISZTINA M.
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES USING
; INFORMATION: CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,777
; FILING DATE: 29-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDEL, SARALYNN
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: CELL20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)358-9600 X345
; TELEFAX: (415)349-7392
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-412-777-2
;
Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAA 29
Db 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 14
US-08-412-826-1/c
; Sequence 1, Application US/08412826
; Patent No. 6130364
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: ZSEBO, KRISZTINA M.
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES USING
; INFORMATION: CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,826
; FILING DATE: 29-MAR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDEL, SARALYNN
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: CELL21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)358-9600 X345
; TELEFAX: (415)349-7392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-412-826-1
;
Query Match 85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 34 ATAACCTTCGTATAGCATACATTATACGAA 6

RESULT 15
US-08-412-826-2/c
; Sequence 2, Application US/08412826
; Patent No. 6130364
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Fri Sep 9 08:29:51 2005

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; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: ZSEBO, KRISTINA M.
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES USING
; TITLE OF INVENTION: CRE-MEDIATED SITE-SPECIFIC RECOMBINATION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/412,826
; FILING DATE: 29-MAR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: MANDEL, SARALYNN
; REGISTRATION NUMBER: 31,853
; REFERENCE/DOCKET NUMBER: CELL21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)358-9600 X345
; TELEFAX: (415)349-7392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-412-826-2

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Query Match      85.3%; Score 29; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ATAACCTTCGTATAGCATACATTATACGAA 29
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Db      34 ATAACCTTCGTATAGCATACATTATACGAA 6

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Job time : 69 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 20:55:38 ; Search time 309 Seconds
(without alignments)
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Title: US-10-030-658B-16

Perfect score: 34
Sequence: 1 ataacttcgtatagcattacattacgaacgta 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	10	US-09-957-660-2
2	34	100.0	34	14	US-10-118-231-18
3	34	100.0	34	14	US-10-214-722-1
4	34	100.0	34	18	US-10-416-995-10
5	34	100.0	34	19	US-10-739-769-2
6	34	100.0	34	20	US-10-448-395-8
7	34	100.0	34	20	US-10-448-395-14

c	8	34	100.0	40	20	US-10-448-395-17	Sequence 17, Appl
	9	34	100.0	40	20	US-10-448-395-18	Sequence 18, Appl
	10	34	100.0	44	14	US-10-214-722-14	Sequence 14, Appl
c	11	34	100.0	67	14	US-10-214-722-12	Sequence 12, Appl
c	12	34	100.0	75	22	US-10-916-082-10	Sequence 10, Appl
	13	34	100.0	94	14	US-10-118-231-10	Sequence 10, Appl
	14	34	100.0	94	14	US-10-118-231-16	Sequence 16, Appl
c	15	34	100.0	102	22	US-10-916-082-12	Sequence 12, Appl
	16	34	100.0	2133	20	US-10-448-395-1	Sequence 1, Appl
	17	32.4	95.3	34	14	US-10-214-722-2	Sequence 2, Appl
	18	30.8	90.6	34	14	US-10-214-722-3	Sequence 3, Appl
c	19	30.8	90.6	34	19	US-10-739-769-6	Sequence 6, Appl
	20	29.2	85.9	34	14	US-10-214-722-4	Sequence 4, Appl
c	21	29	85.3	34	9	US-09-829-507-1	Sequence 1, Appl
c	22	29	85.3	34	9	US-09-829-507-2	Sequence 2, Appl
c	23	29	85.3	34	9	US-09-920-932-1	Sequence 1, Appl
c	24	29	85.3	34	9	US-09-908-305-3	Sequence 3, Appl
	25	29	85.3	34	9	US-09-908-305-4	Sequence 4, Appl
	26	29	85.3	34	9	US-09-804-653-4	Sequence 4, Appl
c	27	29	85.3	34	9	US-09-804-653-6	Sequence 6, Appl
	28	29	85.3	34	9	US-09-822-634-3	Sequence 3, Appl
c	29	29	85.3	34	9	US-09-945-952A-4	Sequence 4, Appl
c	30	29	85.3	34	10	US-09-948-193-3	Sequence 3, Appl
	31	29	85.3	34	10	US-09-377-885A-1	Sequence 1, Appl
c	32	29	85.3	34	10	US-09-377-885A-20	Sequence 20, Appl
	33	29	85.3	34	10	US-09-981-397A-6	Sequence 6, Appl
c	34	29	85.3	34	10	US-09-997-209-29	Sequence 29, Appl
	35	29	85.3	34	10	US-09-990-185-7	Sequence 7, Appl
	36	29	85.3	34	10	US-09-957-660-1	Sequence 1, Appl
	37	29	85.3	34	10	US-09-957-660-4	Sequence 4, Appl
	38	29	85.3	34	10	US-09-975-304-1	Sequence 1, Appl
c	39	29	85.3	34	10	US-09-843-150-52	Sequence 52, Appl
	40	29	85.3	34	10	US-09-843-150-53	Sequence 53, Appl
c	41	29	85.3	34	13	US-10-072-047-1	Sequence 1, Appl
c	42	29	85.3	34	13	US-10-072-047-2	Sequence 2, Appl
c	43	29	85.3	34	13	US-10-057-050-2	Sequence 2, Appl
c	44	29	85.3	34	14	US-10-081-771-1	Sequence 1, Appl
c	45	29	85.3	34	14	US-10-081-771-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-957-660-2
; Sequence 2, Application US/09957660
; Publication No. US20030100077A1
; GENERAL INFORMATION:
; APPLICANT: KORTE, JOHN A.
; APPLICANT: LOWE, BRENDA A.
; TITLE OF INVENTION: IN VITRO METHOD TO CREATE CIRCULAR MOLECULES FOR USE IN
; TITLE OF INVENTION: TRANSFORMATION
; FILE REFERENCE: DEMO:17605
; CURRENT APPLICATION NUMBER: US/09/957,660
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-957-660-2

Query Match 100.0%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATAACCTTCGTATAGCATTACATTATACGAACGGTA 34
Db 1 ATAACCTTCGTATAGCATTACATTATACGAACGGTA 34

RESULT 2
US-10-118-231-18
; Sequence 18, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Construct
US-10-118-231-18

Query Match 100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34
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DB 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34

RESULT 3
US-10-214-722-1
; Sequence 1, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombinase-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 66 without flanks
US-10-214-722-1

Query Match 100.0%; Score 34; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34
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DB 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34

RESULT 4
US-10-416-995-10

; Sequence 10, Application US/10416995
; Publication No. US20040077089A1
; GENERAL INFORMATION:
; APPLICANT: Xin, Hong-Bo
; APPLICANT: Kotlikoff, Michael
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: VECTORS FOR CONDITIONAL GENE INACTIVATION
; FILE REFERENCE: 1153.020US1
; CURRENT APPLICATION NUMBER: US/10/416,995
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: PCT/US01/43916
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,200
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A mutant loxP sequence
US-10-416-995-10

Query Match 100.0%; Score 34; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34

RESULT 5
US-10-739-769-2
; Sequence 2, Application US/10739769
; Publication No. US20040137624A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; TITLE OF INVENTION: Methods of Site-Directed Transformation
; FILE REFERENCE: 38-15(52823)B
; CURRENT APPLICATION NUMBER: US/10/739,769
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: variant of wild type loxP recombinase site
US-10-739-769-2

Query Match 100.0%; Score 34; DB 19; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34
|||||
DB 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34

RESULT 6
US-10-448-395-8
; Sequence 8, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Aekew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; TITLE OF INVENTION: Using an Inducible Gene Silencer
; FILE REFERENCE: 01997.026400

; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-8

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
|||||
DB 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34

RESULT 7

US-10-448-395-14/c

; Sequence 14, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT FILING DATE: 2003-05-30
; CURRENT APPLICATION NUMBER: US/10/448,395
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic nucleic acid
US-10-448-395-14

Query Match 100.0%; Score 34; DB 20; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
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DB 34 ATAACCTTCGTATAGCATACATTATACGAACGGTA 1

RESULT 8

US-10-448-395-17/c

; Sequence 17, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:

; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-17

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 39 ATAACCTTCGTATAGCATACATTATACGAACGGTA 6

RESULT 9

US-10-448-395-18

; Sequence 18, Application US/10448395
; Publication No. US20040241851A1
; GENERAL INFORMATION:
; APPLICANT: Askew, G. Roger
; APPLICANT: Kanki, Kim L
; APPLICANT: Barton, Michael
; TITLE OF INVENTION: Conditional Knockout Method for Gene Trapping and Gene Targeting
; FILE REFERENCE: 01997.026400
; CURRENT APPLICATION NUMBER: US/10/448,395
; CURRENT FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-448-395-18

Query Match 100.0%; Score 34; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0006;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
|||||
DB 6 ATAACCTTCGTATAGCATACATTATACGAACGGTA 39

RESULT 10

US-10-214-722-14

; Sequence 14, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; TITLE OF INVENTION: consecutive recombine-mediated recombinations
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide lox 66 with flanks
US-10-214-722-14

Query Match 100.0%; Score 34; DB 14; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
Db 6 ATAACCTTCGTATAGCATACATTATACGAACGGTA 39

RESULT 11
US-10-214-722-12/c
; Sequence 12, Application US/10214722
; Publication No. US20030082723A1
; GENERAL INFORMATION:
; APPLICANT: GSF-Forschungszentrum f. Umwelt und Ges. GmbH
; TITLE OF INVENTION: The use of mutated recognition sequences for multiple
; FILE OF INVENTION: consecutive recombinase-mediated recombination
; TITLE OF INVENTION: in a genetic system
; FILE REFERENCE: P14567
; CURRENT APPLICATION NUMBER: US/10/214,722
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: DE 101 40 030.6
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 67
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-214-722-12
Query Match 100.0%; Score 34; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
Db 43 ATAACCTTCGTATAGCATACATTATACGAACGGTA 10

RESULT 12
US-10-916-082-10/c
; Sequence 10, Application US/10916082
; Publication No. US20050153392A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: van Schooten, Wim
; TITLE OF INVENTION: Improved Transgenesis with Humanized
; FILE OF INVENTION: Immunoglobulin Loci
; FILE REFERENCE: 39691-0008
; CURRENT APPLICATION NUMBER: US/10/916,082
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: 60/494,30
; PRIOR FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-916-082-10
Query Match 100.0%; Score 34; DB 22; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
Db 50 ATAACCTTCGTATAGCATACATTATACGAACGGTA 17

RESULT 13
US-10-916-082-12/c
; Sequence 16, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-118-231-16
Query Match 100.0%; Score 34; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
Db 10 ATAACCTTCGTATAGCATACATTATACGAACGGTA 43

RESULT 14
US-10-118-231-16
; Sequence 16, Application US/10118231
; Publication No. US20030005478A1
; GENERAL INFORMATION:
; APPLICANT: Bigger, Brian W
; APPLICANT: Tolmachov, Oleg
; APPLICANT: Coutelle, Charles
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 102286.141US
; CURRENT APPLICATION NUMBER: US/10/118,231
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/327,029
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0108968.9
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-118-231-16
Query Match 100.0%; Score 34; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAACCTTCGTATAGCATACATTATACGAACGGTA 34
Db 10 ATAACCTTCGTATAGCATACATTATACGAACGGTA 43

RESULT 15
US-10-916-082-12/c
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; Sequence 12, Application US/10916082
; Publication No. US2005015392A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Van Schooten, Wim
; TITLE OF INVENTION: Improved Transgenesis with Humanized
; TITLE OF INVENTION: Immunoglobulin Loci
; FILE REFERENCE: 39691-0008
; CURRENT APPLICATION NUMBER: US/10/916,082
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: 60/494,30
; PRIOR FILING DATE: 2003-08-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-916-082-12
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Query Match 100.0%; Score 34; DB 22; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATAACTTCGTATAGCATACATTATACGACGGTA 34
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Db 84 ATAACTTCGTATAGCATACATTATACGACGGTA 51
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Job time : 310 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 22:19:49 ; Search time 1585.5 Seconds
(without alignments)
816.263 Million cell updates/sec

Title: US-10-030-658B-16

Perfect score: 34
Sequence: 1 ataacttgtagcattacattacgaacgta 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gsa1:*

9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.4	92.4	126	BF243776	BF243776 601877514
2	31.4	92.4	530	CF978786	CF978786 2-14-F03
3	31	91.2	747	CF976774	CF976774 2-12-E11
4	30.8	90.6	77	BF382292	BF382292 601815207
5	30.8	90.6	85	BF132923	BF132923 601646101
6	30.8	90.6	88	BF246996	BF246996 601854389
7	30.8	90.6	92	BF238541	BF238541 601904868
8	30.8	90.6	94	BF239393	BF239393 601906694
9	30.8	90.6	97	BF243354	BF243354 601878528
10	30.8	90.6	98	BF241277	BF241277 601878794
11	30.8	90.6	99	BF244775	BF244775 601864535
12	30.8	90.6	100	BF209290	BF209290 601872506
13	30.8	90.6	100	BF213664	BF213664 601847504
14	30.8	90.6	102	BF687672	BF687672 602066704
15	30.8	90.6	106	BF244968	BF244968 601864380
16	30.8	90.6	108	BF240116	BF240116 601905618
17	30.8	90.6	124	BF214305	BF214305 601848531
18	30.8	90.6	130	BF674203	BF674203 602136932
19	30.8	90.6	132	BF977130	BF977130 602146859
20	30.8	90.6	134	BF571954	BF571954 602078272
21	30.8	90.6	135	BF214021	BF214021 601847936
22	30.8	90.6	142	BF247576	BF247576 601858626
23	30.8	90.6	142	BF541761	BF541761 602068101
24	30.8	90.6	144	BF674320	BF674320 602137061

25	30.8	90.6	145	2	BF213890	BF213890 601848120
26	30.8	90.6	147	2	BF245810	BF245810 601864716
27	30.8	90.6	149	2	BF244784	BF244784 601864548
28	30.8	90.6	152	2	BF573591	BF573591 602077358
29	30.8	90.6	161	2	BF243567	BF243567 601879377
30	30.8	90.6	166	4	BF977946	BF977946 602148418
31	30.8	90.6	169	2	BF208812	BF208812 601872302
32	30.8	90.6	177	4	BF977761	BF977761 602148383
33	30.8	90.6	268	7	CF978843	CF978843 2-32-G09
34	30.8	90.6	275	7	CF979148	CF979148 2-18-E07
35	30.8	90.6	282	7	CF978512	CF978512 2-27-F05
36	30.8	90.6	320	7	CF978536	CF978536 2-25-E12
37	30.8	90.6	368	7	CF977378	CF977378 2-25-C02
38	30.8	90.6	374	7	CF978446	CF978446 2-25-E06
39	30.8	90.6	431	7	CF978592	CF978592 2-98-D02
40	30.8	90.6	451	2	BF211083	BF211083 601872840
41	30.8	90.6	455	7	CF978658	CF978658 2-32-F03
42	30.8	90.6	481	4	BF485698	BF485698 602502544
43	30.8	90.6	524	7	CF978902	CF978902 2-26-H12
44	30.8	90.6	535	8	AQ060250	AQ060250 CIT-HSP-2
45	30.8	90.6	623	2	BF573795	BF573795 602079494

ALIGNMENTS

RESULT 1
LOCUS BF243776
DEFINITION 601877514F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105874 5', mRNA linear EST 14-NOV-2000
ACCESSION BF243776
VERSION BF243776.1 GI:11157706
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 126)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM984 row: 1 column: 03
High quality sequence start: 43
High quality sequence stop: 126.
Location/Qualifiers
1. 126
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4105874"
/tissue type="from acute myelogenous leukemia"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH_MGC_55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGAGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length

FEATURES

source

clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

```

ORIGIN
Query Match          92.4%; Score 31.4; DB 2; Length 126;
Best Local Similarity 94.1%; Pred. No. 0.011;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGACGGTA 34
    |||||
Db 84 ATAACCTCGTATAGCATACATTATACGACGGTA 117
    |||||

RESULT 2
CF978786
LOCUS
DEFINITION
2-14-F03.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
sequence.
CF978786
ACCESSION
CF978786.1 GI:49174244
VERSION
CF978786
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 530)
REFERENCE
Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
AUTHORS
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
TITLE
Cells
JOURNAL
Unpublished (2003)
COMMENT
Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
Location/Qualifiers
1. .530
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site 1: SfiI; Site_2:
SfiI; The library was constructed from purified rat
retinal ganglion cells. The Creator SMART cDNA library
method (Clontech) was used. EST analysis was performed on
the unamplified, non-normalized, non-subtracted library."

FEATURES
source
1. .530
Query Match          92.4%; Score 31.4; DB 7; Length 530;
Best Local Similarity 94.1%; Pred. No. 0.012;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGACGGTA 34
    |||||
Db 13 ATAACCTCGTATAGCATACATTATACGACGGTA 46
    |||||

RESULT 3
CF976774
LOCUS
DEFINITION
2-12-E11.F Rat retinal ganglion cell Rattus norvegicus cDNA, mRNA
sequence.
CF976774
ACCESSION
CF976774.1 GI:49172232
VERSION
CF976774
KEYWORDS
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 747)
REFERENCE
Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
AUTHORS
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion
TITLE
Cells
JOURNAL
Unpublished (2003)
COMMENT
Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
Location/Qualifiers
1. .747
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site 1: SfiI; Site_2:
SfiI; The library was constructed from purified rat
retinal ganglion cells. The Creator SMART cDNA library
method (Clontech) was used. EST analysis was performed on
the unamplified, non-normalized, non-subtracted library."

FEATURES
source
1. .747
Query Match          91.2%; Score 31; DB 7; Length 747;
Best Local Similarity 93.9%; Pred. No. 0.018;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGACGGT 33
    |||||
Db 14 ATAACCTCGTATAGCATACATTATACGACGGT 46
    |||||

RESULT 4
BF382292
LOCUS
DEFINITION
60181520752 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:404948 5',
mRNA sequence.
BF382292
ACCESSION
BF382292
VERSION
BF382292.1 GI:11363595
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 77)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW881 row: m column: 01
High quality sequence start: 6
High quality sequence stop: 77.
Location/Qualifiers
1. .77
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source
1. .77

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 747)
Farkas,R.H., Qian,J., Goldberg,J.L., Quigley,H.A. and Zack,D.J.
Gene Expression Profiling of Highly Purified Rat Retinal Ganglion Cells

Unpublished (2003)
Contact: Farkas RH
Department of Ophthalmology
Johns Hopkins University School of Medicine
600 North Wolfe Street, Baltimore, MD 21287, USA
Tel: 410 502 5230
Fax: 410 502 5382
Email: rfarkas@jhmi.edu.
Location/Qualifiers

1. .747
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="Retinal Ganglion Cells"
/lab_host="DH10B"
/clone_lib="Rat retinal ganglion cell"
/note="Organ: Eye; Vector: pDNR-LIB; Site 1: SfiI; Site_2: SfiI; The library was constructed from purified rat retinal ganglion cells. The Creator SMART cDNA library method (Clontech) was used. EST analysis was performed on the unamplified, non-normalized, non-subtracted library."

ORIGIN

Query Match 91.2%; Score 31; DB 7; Length 747;
Best Local Similarity 93.9%; Pred. No. 0.018;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATAACCTCGTATAGCATACATTATACGACGGT 33
 |||||
Db 14 ATAACCTCGTATAGCATACATTATACGACGGT 46
 |||||

RESULT 4

BF382292
LOCUS
DEFINITION
60181520752 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:404948 5',
mRNA sequence.
BF382292
ACCESSION
BF382292
VERSION
BF382292.1 GI:11363595
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 77)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCW881 row: m column: 01
High quality sequence start: 6
High quality sequence stop: 77.
Location/Qualifiers

FEATURES

source
1. .77
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="IMAGE:4049448"
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 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_56"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc);
 Double-stranded cDNA was prepared from cell line RNA.
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 77;
 Best Local Similarity 94.1%; Pred. No. 0.018;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
 |||||
 Db 24 ATAACTTCGTATAGCATACATTATACGAAGTTA 57
 |||||

RESULT 5

BF132923

LOCUS

DEFINITION

601646101F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4101792 5',

mRNA sequence.

BF132923

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence start: 12

High quality sequence stop: 85.

Location/Qualifiers

1. .85

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4101792"

/tissue_type="mucoepidermoid carcinoma"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_59"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:

SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc);

Double-stranded cDNA was prepared from cell line RNA.

and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3'

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 85;
 Best Local Similarity 94.1%; Pred. No. 0.018;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
 |||||
 Db 52 ATAACTTCGTATAGCATACATTATACGAAGTTA 85
 |||||

RESULT 6

BF246996

LOCUS

DEFINITION

BF246996 88 bp mRNA linear EST 14-NOV-2000

mRNA sequence.

BF246996

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC924 row: a column: 24

High quality sequence start: 19

High quality sequence stop: 88.

Location/Qualifiers

1. .88

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4074143"

/tissue_type="glioblastoma"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_57"

/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:

SfiI (ggccctcgcc); Site_2: SfiI (ggccattggcc);

Double-stranded cDNA was prepared from cell line RNA.

and 3' adaptors were used in cloning as follows: 5'

adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3'

(where B = A, C, or G and N = A, C, G, or T). Average

insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies

contained inserts by PCR. This library was enriched for

full-length clones and was constructed by Clontech

Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 90.6%; Score 30.8; DB 2; Length 88;
 Best Local Similarity 94.1%; Pred. No. 0.018;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACTTCGTATAGCATACATTATACGAACGGTA 34
 |||||
 Db 35 ATAACTTCGTATAGCATACATTATACGAAGTTA 68
 |||||

RESULT 7

FEATURES	High quality sequence stop: 97.		source	
	Location/Qualifiers			
	1. .97			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:4107295"			
	/tissue_type="from acute myelogenous leukemia"			
	/lab_host="DH10B (T1 phage-resistant)"			
	/clone_lib="NIH_MGC_55"			
	/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."			
ORIGIN	Query Match		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	RESULT 10		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	Query Match		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	RESULT 10		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	Query Match		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	RESULT 10		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	Query Match		90.6%; Score 30.8; DB 2; Length 97;	
	Best Local Similarity			
	Matches	32; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
	QY			
	1 ATAACCTTCGTATAGCATACATTATACGACGGTA 34			
	Db	55 ATAACCTTCGTATAGCATACATTATACGACGGTTA 89		
ORIGIN	Query Match		90.6	

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QY 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34
Db 57 ATAACCTCGTATAGCATACATTATACGAAGGTTA 90

RESULT 12
BF209290
LOCUS
DEFINITION 601872506F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4096633 5',
ACCESSION BF209290
VERSION BF209290.1 GI:11102876
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 100)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM935 row: g column: 02
High quality sequence start: 6
High quality sequence stop: 100.
Location/Qualifiers
1..100
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4096633"
/tissue type="from chronic myelogenous leukemia"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH_MGC_54"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfII (ggcgcttcggcc); Site 2: SfII
(ggcattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCGGCGCGGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
```

ORIGIN

```

Query Match 90.6%; Score 30.8; DB 2; Length 100;
Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATAACCTCGTATAGCATACATTATACGAACGGTA 34
Db 47 ATAACCTCGTATAGCATACATTATACGAAGGTTA 80

RESULT 14
BF687672
LOCUS
DEFINITION 602066704F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065817 5',
ACCESSION BF687672
VERSION BF687672.1 GI:11973080
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 102)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LICM902 row: 9 column: 02
 High quality sequence start: 12
 High quality sequence stop: 102.

FEATURES

source

```

1. .102
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4065817"
/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_57"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCACATG-dT(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
```

ORIGIN

```

Query Match      90.6%; Score 30.8; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY      1  ATAACTTCGTATAGCATACATTATACGAACGTA 34
         |||||
Db      49  ATAACTTCGTATAGCATACATTATACGAAGTTA 82
```

RESULT 15

```

BF244968      106 bp mRNA linear EST 14-NOV-2000
LOCUS      601864380F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4082923 5',
DEFINITION      mRNA sequence.
ACCESSION      BF244968
VERSION      BF244968.1 GI:11158900
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 106)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
```

```

cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM946 row: 0 column: 20
High quality sequence start: 10
High quality sequence stop: 106.
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FEATURES

source

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1. .106
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4082923"
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```

/tissue_type="glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_57"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCACATG-dT(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
```

ORIGIN

```

Query Match      90.6%; Score 30.8; DB 2; Length 106;
Best Local Similarity 94.1%; Pred. No. 0.019;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```

QY      1  ATAACTTCGTATAGCATACATTATACGAACGTA 34
         |||||
Db      53  ATAACTTCGTATAGCATACATTATACGAAGTTA 86
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 Job time : 1587.5 secs

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